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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

- protein search, using sw model OM protein Мау Run on:

1, 2003, 07:49:49 ; Search time 39.3958 Seconds
(without alignments)
412.647 Million cell updates/sec

Title:

US-09-987-485-1 615 1 MKLKVIVNGTAYDVDVDVDK.......KVLVKERDAVQGQGLIKIĘ Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

908470

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Database :

/SIDS2/gcgdata/geneseq/genesec/ /SIDS2/gcgdata/geneseq/genesec A_Geneseq_101002:*

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT: /gcgdata/geneseg/genesegp-embl/AA1980.DAT: DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984./SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985./SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986./SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.l/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.l/ /gcgdata/geneseg/genesegp-embl/AA1998 /qcqdata/qeneseq/qeneseqp-embl/AA2001 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993 gcgdata/geneseq/geneseqp-embl/AA1995 /qcqdata/qeneseq/qeneseqp-embl/AA1997 /denesedp 'SIDS2/gcgdata/geneseq/geneseqp /gcgdata/geneseg/genesegp cqdata/qenesed/qenesedp /SIDS2/gcgdata/geneseg SIDS2 IDS: SIDS:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Amino acid sequenc Outer surface prot Hantavirus nuclear Amino acid sequenc Amino acid sequenc 1.35 polypeptide o Prophonibacterium Putative biotin ca Oxalacetate decarb Corynebacterium th
ΠD	AAY84002 AAY78908 AAX11886 AAX84001 AAX84001 AAX8177 AAX11122 AAB96610 AAR42120 AAB3169
DB	22 22 23 24 25 25
å Ouery Match Length DB	126 126 255 266 123 125 148 100
% Query Match	100.0 100.0 100.0 100.0 100.0 98.3 70.9 37.6 31.5
Score	615 615 615 615 615 615 604.5 436 231.5 1193.5
Result No.	H10-4-10-00 0 0 0 0 0 0

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AAU001126 AAG93186 AAA939174 AAU98050 AAB8180 AAB8180 AAB8180 AAB72299 AAB79299 AAG93249 AAG93249 AAG93249 AAU30712 AAG93211 AAG93249 AAU3072	
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Human colon cancer Human ovarian anti Novel human diagno Human polypeptide Staptinococus epi Chlamydia pneumoni S. epidermidis ope Staphylococus epi Propionibacterium Arabidopsis thalia	ALIGNMENTS				pallidum protein.	gen; membrane antigen; syphilis.								anti-Treponema pallidum antibodies, used for diagnosis g a fusion protein of membrane antigen with peptide n be biotinylated in vivo	н.	The present sequence represents a Treponema pallidum protein, which is used to produce a fusion protein antigen for use in the method of aftereting antibodies against Treponema pallidum. The antibodies are detected in a sample by reaction with a fusion protein antigen, present in the mixture in Inhalting concentration. The fusion protein antigen comprises a Treponema pallidum membrane antigen. The method is used for diagnosis of syphilis.	
AAG75011 ABE11217 AAM39515 AAM41301 AAE612301 AAE09858 AAE09858 AAE1317 AAG17822 AAG17822 AAG17822 AAG17822 AAG17822 AAG17822	ALIGN	126 AA.			pallidum	ein antigen;						.00		Treponema pallic usion protein of biotinylated in	Disclosure; Page 12–13; 16pp; English	nts a Tre tein ant tion desc pallidur a fusion entration um membra	
222 222 222 223 223 221 221 221 221 221		in;		γ)	E	protein				877.	920.	45	A	pone on p	16pp	rese pro fica fica nema with conc conc s.	
76 76 77 72 72 72 72 73 74 74 74 76 76 76 76 76 76 76 76 76 76 76 76 76		standard; Protein;		st entry)	ice of a	fusion	ë			99EP-0115877	98US-0148920	BECTON DICKINSON	Deutsch In 57/20. 47.	nti-Tre rafusi bebio	12-13;	sequence represents uce a fusion protein . The specification gainst Treponema pa. by reaction with a in limiting concent. Treponema pallidum rs of syphilis.	-
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		stan		00		vector;	pal	SS.	. 00	66;	98;	ECTO	KG0 -226 AZ99	ay f is u that	e;	nt s rodu tion s ag le b le b re i a T	1
110 110 110 110 110 108 108 108 108 108		84002	AAY84002;	03-JUL-2000	Amino acid	PinPoint	Treponema pallidum	BP968931 -02	5-MAR-2000	2-AUG-1999	4-SEP-1998;	(BECT) B	Krillenik KG, Berks WPI; 2000-226057/20 N-PSDB; AA299247.	Immunoassay for a of syphilis using sequence that can	isclosur	The present sequused to produce the invention. T antibodies again in a sample by r the mixture in 1 comprises a Trep for diagnosis of sequence 126 A	anianhae
8888888888888888888888888888888901		SUL r84					VY OS CS		7	PF 12	PR 04		The Park		PS D		

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(05pC) Drail fragment amino acid sequence. The polypeptide contains an immunological epitope used in the invention. Large amounts of Ospc are infected ticks to mammalian hosts. The Ospc protein sequence is used to dispose B. Dorrelian hosts. The Ospc protein sequence is used to dispose B. Dorrelia infection in mammals. The Ospc nuclectide sequence is used to prevent (via vaccination), treat or detect Borrelia (sepecially B. burgdorferi) infections, i.e. Lyme disease, in mammals including humans. The Ospc nuclectides a superior classostic antigen that detects early Lyme disease infection, predicts successful eradication or the organism from the host, and discriminates between individuals with Lyme disease and individuals who have been vaccinated with an Osph Lyme disease vaccination. Detection of anti-Ospc correliacidal antibodies advantageously gives an early diagnosis which anti-Ospc borreliacidal antibodies advantageously gives an early diagnosis which anti-Ospa muth Ospa, vaccination with Ospc results in clearance of spirochetes and resolution of symptoms even if administered after
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the Borrella burgdorferi outer surface protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New immunogenic polypeptides useful as a vaccine against Lyme disease and for treating and detecting borrelia infection in mammals consists an epitope of Borrella burgdorferl OspC fragment
                                                                     AGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIK 120
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Outer surface protein C (OspC) DraI fragment amino acid sequence.
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100.0%; Pred. No. 4.1e-52;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                          AAY78908 standard; Protein; 194 AA.
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N-PSDB; AAZ92216.
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100.0%; Score 615; DB 21; Length 126; llarity 100.0%; Pred. No. 2.4e-52; Conservative 0; Mismatches 0; Indels 0

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Matches 122;
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                                                                                                                                                                                                                                                                                                                  (ATAT-)
(ARIK/)
                                                                                                                                                         Sequence
                                                                                                                                                                                                                                     Example 1; Page 17; 18pp; Japanese.
                                                                                                                                                                                                                                                       diagnosis
                                                                                                                                                                                                                                                       Hantavirus antigen protein and monoclonal antibody - diagnosis and treatment of hantavirus infection
                                                                                                                                                                                                                                                                                     WPI; 1997-083468/08
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) ARIKAWA J.
) HASHIMOTO N.
122
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Pred. No. 5.7e-52;
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RESULT

Amino acid sequence of a T.

pallidum membrane

protein antigen

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AAY84001
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Matches 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoassay for anti-Treponema pallidum antibodies, used for diagnosis of syphilis using a fusion protein of membrane antigen with peptide sequence that can be biotinylated in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 10-11; 16pp; English.
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                                                                             AAY84003 standard;
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                                                                                                                                                                                         Propionibacterium shermanii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BECT ) BECTON DICKINSON & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e present sequence represents a Treponema pallidum membrane protein tigen, which is used to produce a fusion protein antigen for use the method of the invention. The specification describes a method of detecting antibodies against Treponema pallidum. The antibodies e detected in a sample by reaction with a fusion protein antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLKVTVNGTAYDVDVDVDKSHENPMGTILFGGGTGGAPAPAAGGAGAGKAGEGEIPAPL
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                                                                                                                                                                                                                                                    lnding; biotin; protein
chromatography.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                            Location/Qualifiers 58..100
                                                        /label= biotin-binding_recognition_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ample by reaction with a fusion protein antigen, ure in limiting concentration. The fusion protein Treponema pallidum membrane antigen. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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Pred. No. 6e-52;
                                                                                                                                                                                                                                                                                  purification;
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Best Local :
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        21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The P.shermanii 1.3S polypeptide is a preferred avidin-binding polypeptide for inclusion in the recombinant hybrid polypeptide the invention. In the hybrid, a polypeptide of interest is fused the C-terminus of the avidin-binding polypeptide. The hybrid polypeptide can then be recovered in a single chromatographic stusing avidin monomer affinity chromatography.
                                                 20-APR-2001;
                                                                      01-NOV-2001
                                                                                          WO200181581-A2
                                                                                                              Propionibacterium
                                                                                                                                  dermatological;
                                                                                                                                            uveitis; endophthalmitis; inflammatory lesion; acne
                                                                                                                                                        uveitis;
                                                                                                                                                                 SAPHO
                                                                                                                                                                                    Propionibacterium acnes immunogenic protein #12018.
                                                                                                                                                                                                         27-FEB-2002
                                                                                                                                                                                                                               AAU51122;
                                                                                                                                                                                                                                                   AAU51122 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 23; 40pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                              122;
                                                                                                                                                                syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide - contains a polypeptide fus
g polypeptide contg. a biotin attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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       ; 2000US-199047P.
; 2000US-208841P.
; 2000US-216747P.
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                                                 2001WO-US12865
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                                                                                                                                 osteopathic;
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                                                                                                                                                                synovitis;
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                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                       98.3%;
99.2%;
                                                                                                                                            ; acne; pustulosis; hypertosis
bone; joint; central nervous
vulgaris; enzyme linked immur
                                                                                                                                                                                                                                                                                                                                                                                                                            pred. No. 2.4e
0; Mismatches
                                                                                                                                                                                                                                                    125
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No. 2.4e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ent domain
                                                                                                                                                              hypertosis; osteomyelitis;
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                                                                                                                                                     system;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification, at ftp.wire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides. The proteins and their associated DNA sequences the treatment, prevention and diagnosis of medical conditions P. acnes. The disorders include SAPHO syndrome (synovitis, acr
 21-APR-1999;
                                 27-OCT-2000
                                                                 FR2792651-A1
                                                                                               Pyrococcus abyssi.
                                                                                                                             Hyperthermophilic archaeon;
                                                                                                                                                            Putative biotin carboxylase
                                                                                                                                                                                             29-OCT-2001
                                                                                                                                                                                                                             AAB96610;
                                                                                                                                                                                                                                                           AAB96610 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           presence or absence of P. acres in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating acne vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes vaccinating against and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky YAW, Persing DH, I
L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                           AGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLKVTVNDVAYDVDVDVDKTANAPMAPILFGGGAGG-PMKASGG-GAGKAGEGEVPAPL
                                                                                                                                                                                                                                                                                                                                                                        IG 122
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                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
 99FR-0005034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides and nucleic acids useful diagnosing infections, especially use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                                                                                                                           148
                                                                                                                            hyperthermophilic protein
                                                                                                                                                            carrier protein of acetyl-CoA carboxylase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 436; DB 22;
Pred. No. 6.3e-35;
9; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 125;
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RESULT 9
AAR42120
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41233-7) and P. abyssi proteins. P. abyssi a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up 110 degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 1349; 1657pp; French.
                                                                                                                                                                                                                                                       12-OCT-1993
                                                                                                                                                                                                                                                                                                    US5252466-A.
                                                                                                                                                                                                                                                                                                                                                     Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                        Fusion protein; post-translation modification; biotination; marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxalacetate decarboxylase alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR42120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleotide sequences isolated proteins useful in industry -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Forterre P,
Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1999;
                                             (BIOT-) BIOTECHNOLOGY RES & DEV CORP (UNII ) UNIV ILLINOIS FOUND.
                                                                                                                        19-MAY-1989;
18-MAY-1990;
                                                                                                                                                                                                    18-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR42120 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGKVEKVLVKERDAVQGGQGLIKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTPVQAPTTPQVQASENVVTAPMPGKVLKILVQEGQQVKLGQGLLILEAMKMENEIPAPR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKVKVVVNGKEYEVDVEEVMPGKFRVTLEGKTYEVEANLGIQVAPVQTQVATPAPTPTPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGVVKRILVKEGDAVDTGTPLIELG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thierry JC,
Weissenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                        89US-0354266
90US-0525568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99FR-0005034.
                                                                                                                                                                                                    90US-0525568
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J, Saurin W, Heili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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Pred. No. 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .3e-15;
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RESULT 10
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Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                     04-OCT-1999;
01-NOV-1999;
21-APR-2000;
The present sequence is provided encoding thermophilic amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium; thermophilic; amin thermotolerant; aceA; accBC; dtsRl; pdhA; pc; ppc; acn; icd; lpd; odhA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of a portion of the alpha subunit of pneumoniae oxalacetate decarboxylase. It is used as part oprotein allowing for post-translation biotination which protein allowed the protein allowe
                                                              Claim
                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                               Sugimoto
                                                                                                                                                                                                                                                     Osumi
                                                                                                                                                                                                                                                                        Hirano
                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000; 2000WO-JP06913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium
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                                                                                                                        Proteins and their DNA useful for microbial production of L-amino acids
                                                                                                                                                                                                                                                                                                               (AJIN ) AJINOMOTO CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB83169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB83169 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           marker for the fusion protein that can be used directly or indirectly to identify the fusion protein or to isolate it from a mixt. of other materials such as host cell culture media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1993-336075/42.
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                                                                                                                                                                   2001-300170/31.
DB; AAF87428.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APAPASAPAAAAPAGAGTPVTAPLAGFIWKVLASEGQTVAAGEVLLILEAMKMETEIRAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APAPAAGGAGAGKAGEG-EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP
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                                                              Page 91-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                                                                                                                                                  Matsui
                                                                                                                                                                                                                                                Nonaka G,
Matsui K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100
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; 99JP-0311147.
; 2000JP-0120687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thermoaminogenes
                                                                                                                                                                                                                                                                                                                 INC.
                                                                                                                                                                                                                                                Matsuzaki Y, Akiyoshi N,
Kawahara Y, Kurahashi O,
                                                       215pp; Japanese.
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51.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              te for post-translation modification - used to identify or isolate fusion proteins
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Pred. No. 1.9e-11;
0; Mismatches 30;
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in a specification biosynthesis system
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dtsR2; pfk; scrB; gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein.
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  system
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Nakamatsu
n relating
em enzymes
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gluABCD;
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of a fusion
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RESULT 11
AAU03126
ID AAU03
XX AU03
XX AU03
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XX Crep
XX Virul
KW Gram-
XX W0200
XX W22-DH
XX 22-DH
PR 23-DH
PR 17-FH
PR 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virulence; attenuated microorganism; Gram-positive bacteria; antimicrobia
                                                                    (MICR-) MICROSCIENCE
                                                                                                                                                                                                                                                           17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virulence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 LIKI 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KLKVTVNGTAYDVDVDVDKSHENPMGTILFGGGTGGAPAP----AAGGAGAGKAGEGEIP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLEI 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQG
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                     EE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     591 AA;
                        Zhou
                                                                                                                                                                                                          2000GB-0003729.
2000GB-0003739.
2000GB-0003730.
2000GB-0003731.
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2000GB-0003726.
2000GB-0003727.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-GB04997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pyogenes virulence protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 174; DB 22; Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GDLALGGGAGAAKKKPKKRRAGGAKAGVSGD-SVA 526
                     Feldman
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A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcal infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          impetigo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                     Holden
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 591;
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                     P
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RESULT 12
AAG93186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC AAU03119-AAU03149 represent novel Streptococcus pyogenes virulence
CC proteins #1-31. The S. pyogenes virulence genes can be used to
CC produce attenuated microorganisms comprising a mutation that disrupt
CC the expression of the virulence protein. The virulence genes, proteins
CC or an attenuated microorganism are useful for therapeutic or diagnostic
CC purposes. DNA encoding the virulence proteins, the proteins themselves,
CC an attenuated microorganism or a vaccine comprising the virulence
CC protein are useful for the manufacture of a medicament for use in
CC the treatment or prevention of a condition associated with infection
CC by Streptococcal or Gram positive bacteria, for veterinary treatment,
CC and in a screening assay for the identification of an antimicrobial
CC drug. Discorders which can be treated using S. pyogenes virulence
CC polynucleotide and polypeptide sequences include non-invasive infections
CC and invasive infections e.g. impetigo, pharyngitis, necrotising
CC fascilitis, bacteraemia, streptococcal toxic shock syndrome (STSS),
CC pneumonia and rheumatic fever. The virulence proteins are also useful
CC in the preparation of antihodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                          16-DEC-1999;
07-APR-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                 Coryneform bacterium; organic acid synthesi:
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or preventing a condition associated with ini
Gram-positive bacteria, preferably pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 40-41; 91pp; English.
                                                                                                                                                                                                    Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
            (KYOW ) KYOWA HAKKO
                                                                                                         18-DEC-2000;
                                                                                                                                        20-JUN-2001.
                                                                                                                                                                      EP1108790-A2
                                                                                                                                                                                                                                                                                                               26-SEP-2001
                                                                                                                                                                                                                                                                                                                                             AAG93186
                                                                                                                                                                                                                                                                                                                                                                         AAG93186 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     108
                                                                                                                                                                                                                                                                              glutamicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the preparation of antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGKVEKVLVKERDAVQGGQGLIKIG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTITAIHVGPGQVVNPGDGLITIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLKVTVNGTAYDVDVDVSHENPMGTILFGGGTGGAPAPAAGGA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVEEAQAPQPVAAAGADAIPSPMPGTILKVLVAVGDQVTENQPLLILEAMKMENEIVASS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFKITIDGKEYLVEME----
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B; AAS06358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
                                        99JP-0377484.
2000JP-0159162.
2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPT 97
                                                                                                         2000EP-0127688
                                                                                                                                                                                                                                  synthesis.
                                                                                                                                                                                                                                                                              protein fragment
                                                                                                                                                                                                                                                                                                           (first entry)
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            KOGYO KK
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                                                                                                                                                                                                                                               amino
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15; Mismatches
                                                                                                                                                                                                                                               acid
                                                                                                                                                                                                                                                                              SEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                     132
                                                                                                                                                                                                                                               synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                              ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -EIGAPAQAAAPAQPISTPVPVPTEASP
                                                                                                                                                                                                                                                                              6940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pyogenes useful for treating infection by Streptococcal or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
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SXCCCCCCCCCCCXSXFFFFFXXXXXII
                                                                                                    The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakagawa
Tateishi
Sequence
                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotides derived from Coryneform bacteria, for identi; mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous
                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                    European
                                                                                         particularly L-lysine. The present sequence is in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-376931/40.
                                                                                                                                                                                                                                                                                                29;
                                      Patent Office.
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                                                                                                                                                                                                                                                                                              SEQ ID NO:
 591
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Senoh A,
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                                                                                                                                                                                                                                                                                              6940;
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                                                                                                                                                                                                                                                                                              246pp + Sequence Listing; English
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e, analysing
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                                                                                                                                                                                                                                                                                                                                           RESULT 13
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Best Local S
Matches 48
                                                                                                                                                                 membrane construction and membrane transport protein; petroleum shydrocarbon degradation; gram positive aerobic bacterium; marker; hydrocarbon degradation; fine chemical production; transfoundentification; microorganism; fine chemical production; transfoundentification;
                                                                                                                                                                                                        Corynebacterium glutamicum; brevibacterium
                                                                                                                                                                                                                                   Corynebacterium glutamicum MCT protein SEQ ID
                                                                                                                                                                                                                                                             11-APR-2001
                                                                                                                                                                                                                                                                                        AAB76521;
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                                                                                                                                                                                                                                                                                                                                                                                  LLEI 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLKVTVNGTAYDVDVDKSHENPMGTILFGGGTGGAPAPA----AGGAGAGKAGEGEIP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 38.7
48; Conservative
                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LALGGTAGPKKKAKKRRAGGAKAGVSGDA-VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 170.5; DB 2
Pred. No. 3.1e-08;
6; Mismatches 45
                                                                                                                                                                                                        lactofermentum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                   NO:24.
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                                                                                                                                                                                             spill;
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27.7%; 38.7%;

22;

Length

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25-JUN-1999; 08-JUL-1999; 08-JUL-1999;

99US-0141031. 99DE-1031454. 99DE-1031478.

23-JUN-2000; 04-JAN-2001 WO200100805-A2 Corynebacterium genome mapping;

2000WO-IB00926

glutamicum genetic

engineering

transformation

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Best Local Similarity
Matches 48; Conser
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27-AUG-
31-AUG-
31-AUG-
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27-AUG-
27-AUG-
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27 - AUG-
27 - AUG-
                                                                                                                                                                                                                                                                                                                                                 construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.

AAF68082 and AAF68082 represent sequencing primers which are used in an area of the form of the following contents of the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation -
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                 example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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N-PSDB; AAF67754.
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09-JUL-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pompejus M,
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LIKI 121
                                                                                                                                                                  KLKYTYNGTAYDYDVDKSHENPMGTILFGGGTGGAPAPA----AGGAGAGKAGEGEIP 57
                                                                               APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQG
                                                                                                                         KVVVEINGRRVEVALPGD------LALGGTAGPKKKAKKRRAGGAKAGVSGDA-VA 526
                                           APMQGTVIKVNVEEGAEVNEGDTVVVLEAMKMENPVKAHKSGTVTGLTVAAGEGVNKGVV 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Page 171-173; 1119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASF
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                                                                                                                                                                                                                                                                                             591 AA;
                                                                                                                                                                                                             Conservative
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99DE-1040830

99DE-1040831

99DE-1040832

99DE-1041378

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99DE-1032209.
99DE-1032212.
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99DE-1040765.
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g-1033005.
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38.7%;
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                                                                                                                                                                                                             16;
                                                                                                                                                                                                      Score 170.5; DB 2
Pred. No. 3.1e-08;
6; Mismatches 45
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                                                                                       intervals, (c) PP induces an in vitro response, or in vitro recall response, determined by release of IFN-gamma of at least 1000 pg/ml or 500 pg/ml, respectively, from Peripheral Blood Mononuclear Cells (PBMC) withdrawn from TB patients, or PPD positive individuals, 6 months after diagnosis, (d) PP induces a specific antibody response in a TB patient, as determined by enzyme linked immunosorbent assay (ELISA) technique or a western blot, (e) PP induces a positive delayed type hypersensitivity (DTH) response, determined by intradermal injection. (I) and (II) are useful in preparing a prophylactic or therapeutic medicine as a vaccine for induction of a protective or generation of an immune response in a mammal against infection with a virulent Mycobacterium. (I) and (II) are also useful as diagnostic reagent for the diagnosis of a virulent mycobacterium infection. The vaccine of the invention induces efficient mycobacterium infection.
                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel polypeptide (PP) of somatic proteins extract (I) which have tuberculostatic activity. (I) or their subsequence has at least one of the following properties: (a) the PP induces an in vitro recall response, or an in vitro response, during primary infection with virulent Mycobacterium, determined by a release of interferon (IFN) gamma, (b) PP induces a protective immunity, determined by vaccinating an animal with PP and an adjuvant, three times at two weeks vaccinating an animal with PP and an adjuvant, three times at two weeks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculosis; TB; antigen; vaccine; diagnosis; somatic; tuberculostatic; infection; interferon-gamma; IFN-gamma; protective immunity; therapy; delayed type hypersensitivity response; TB64.
                               immunological memory, providing long term protection against TB. sequence represents a Microbacterium tuberculosis TB64 antigen described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 100-101; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptide of somatic protein extract useful as vaccine against virulent Mycobacterium infection, isolated from cell wall, cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. tuberculosis antigen TB64 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane and cytosol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA39568.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1998;
21-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۵,
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99US-0116673
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P induces an in
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Best Local Similarity Matches 45; Conserv

Conservative

18;

Mismatches

27.0%; Score 166; DB 21; 35.7%; Pred. No. 8.7e-08;

Length 600; Indels

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Query Match

Sequence

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pyruvate carboxylase enzyme. The invention is useful for producing an amino acid (e.g. L-Lys, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro), by culturing a host cell in a suitable media and separating the amino replacement of a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate carboxylase gene, in a Corynebacterium glutamicum, replacing a genomic copy of the wild-type pyruvate carboxylase gene wild-type pyruvate carboxylase yellow wild-type pyruvate carboxylase gene wild-type pyruvate carboxylase yellow wild-type pyruvate carboxylase yellow wild-type pyruvate carboxylase yellow wild-type yellow wild-type yellow wi
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aspartic acid feedba
                                                                                                                                                                                                            Claim 17;
                                                                                                                                                                                                                                                            Novel mutated, feedback resistant pyruvate carboxylase enzyme polypeptide, useful for producing amino acids e.g. L-lysine, L-threonine, L-glycine, L-glutamic acid, L-proline and L-methionine
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                                                                                                                                                                                                          Fig 1;
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217..2;
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                                                                                                                                                                                                          English.
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04-OCT-1999; 01-NOV-1999; 21-APR-2000;

99JP-0282716. 99JP-0311147. 2000JP-0120687.

04-OCT-2000;

2000WO-JP06913

12-APR-2001

Hirano S, Osumi T,

Nonaka G, Matsui K,

Matsuzaki ! Kawahara Y, Kawahara

Y,

Akiyoshi N, Kurahashi O,

Nakamura Nakamatsu

Kimura

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(AJIN) AJINOMOTO CO

Sugimoto

WPI; 2001-300170/31. N-PSDB; AAF87437.

Claim

9;

Page 132-135;

215pp; Japanese

provided in a specification relating

present sequence is

Proteins

and

their DNA useful

for microbial

production

of L-amino

acids

encoding thermophilic amino acid biosynthesis system enzymes of the thermotolerant bacterium Corynebacterium thermoaminogenes. The novel proteins retain at least 30% isocitrate ligase activit after heating at 500c for 5 minutes. DNA fragments encoding the enzymes were isolated from a Corynebacterium thermoaminogenes chromosomal DNA plasmid library by PCR. The DNA may be used for

activity

of t

genes

developing strains of amino acid

producing

microorganisms

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RESULT 16
AAB83180
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ន្គ្រីន្ត្រី
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombination strain, and replacing the selectable marker gene in the first recombinant strain, with feedback resistant pyruvate carboxylase gene through homologous recombination to form a second recombinant strain, where the homologous recombination in the above steps, occurs between the host cell and the vector. The feedback-resistant pyruvate carboxylase enzyme is resistant to feedback inhibition from aspartic acid. The present amino acid sequence represents the feedback-resistant pyruvate carboxylase enzyme of the invention.
                                                                                                                                                                                                                                                                                                                                                                                 pdhA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB83180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1084 ADSSNKGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERVVVP 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                             Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium thermoaminogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-2001
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                                                                                                                                                                                                                                                                                                                                         WO200125447-A1
                                                                                                                                                                                                                                                                                                                                                                                            thermotolerant; aceA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATKVEGGDLIVVV 1156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 44.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein; 1139
                                                                                                                                                                                                                                                                                                                                                                                 ppc;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  acn;
                                                                                                                                                                                                                                                                                                                                                             thermoaminogenes.
                                                                                                                                                                                                                                                                                                                                                                                                      thermophilic; amino
                                                                                                                                                                                                                                                                                                                                                                                 A; accBC; dtsR1;
icd; lpd; odhA.
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                                                                                                                                                                                                                                                                                                                                                                                           dtsR1; dtsR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 162.5; DB
Pred. No. 4.3e-07
4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                          pc protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                         acid biosynthesis; enzyme;
dtsR2; pfk; scrB; gluABCD;
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RESULT 17
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                                                                              14-JUL-1999;
14-JUL-1999;
27-AUG-1999;
31-AUG-1999;
03-SEP-1999;
03-SEP-1999;
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08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                           SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; purlne base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
(BADI )
                                                                                                                                                                       09-JUL-1999;
09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1083
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                                                                                                                                                                                                                                                                                                                                                                           W0200100844-A2
                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum SMP protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB79298 standard; Protein; 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1040 VNVNGQIRPIKVR-DRSVESVTAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-VTVAEGDEIKAGDAVAIIEAMKMEATITAPVDGVIDRVVVPAATKVEGGDLIVVV 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI
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                   99DE-1042088.
99DE-1042095.
99DE-1042123.
99DE-1042125.
                                                 99DE-1042086.
99DE-1042087.
99DE-1042088.
                                                                             99DE-103230.
99US-0143208.
99DE-1032924.
99DE-1032973.
99DE-1033005.
99DE-1040765.
99US-0151572.
99DE-1042076.
99DE-1042079.
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                                                                                                                                                                                           2-1031434.
2-1031510.
2-1031562.
2-1031634.
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Pred. No. 4.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1139;
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or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to C. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARAB73243 to AAB 19033 WHICH the AND TOWN TOWN TOWN TOWN THE C. glutamicum SMP gene can be used in vectors energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as, an organic acid, a proteinogenic production of fine chemicals, such as a proteinogenic production of fine chemicals, such as a proteinogenic production of fine chemicals, and the 
                                                                                  for function, in modulating SMP protein metabolism of sugars, and in modulating in a cell (i.e. ATP, NADPH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carbohydrates or enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metabolism and oxidative phosphorylation AAB79243 to AAB 79633 which are involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pompejus M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to AAF71750 encode the Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 307-308; 1246pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kroeger
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Best Local S
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    258
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AATKVEGGDLIVVV
                      ERDAVQGGQGLIKI
                                    ADSSNKGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVP 257
                                                          AGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107
                                                                                          Similarity
                                                                                Conservative
                       121
    271
                                                                                          25.9%;
43.2%;
                                                                               15;
                                                                                         Score 159.5; DB : Pred. No. 1.4e-07
                                                                                Mismatches
                                                                                                  22;
                                                                               Indels
                                                                                                  Length
                                                                              1;
                                                                              Gaps
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1:

Sequence

272

A

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RESULT
                                                                                                                                SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; purine base; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme
                                                                                                                                                                                                                                  Corynebacterium glutamicum SMP protein sequence
                                                                                                                                                                                                         Corynebacterium glutamicum;
                                                                                                                                                                                                                                                               30-APR-2001
                                                                                                                                                                                                                                                                                          AAB79299;
                                                                                                                                                                                                                                                                                                                   AAB79299 standard;
                                                                                                                         Corynebacterium
                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                   Protein; 272
                                                                                                                                                                                                      carbon metabolism and energy production;
                                                                                                                                                                                                                                  SEQ
                                                                                                                                                                                                                                  IJ
                                                                                                                                                                                                                                  NO:114.
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Corynebacterium

glutamicum

WO200100844-A2

23-JUN-2000; 2000WO-IB00943

04-JAN-2001

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CC energy production. The C glutamicum superior carbon metabolism and ccentry production. The C glutamicum swy gene can be used in vectors cc (II) for expression in host cells and production or modulation of cc production of fine chemicals, such as, an organic acid, a proteinogenic cc or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, cc a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty cc acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cc (III) encoded by them are used for diagnosing the presence or activity of containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms required cc in evolutionary studies, in determining SMP protein regions required cc for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production cc in a cell (i.e. ATP, NADPH).
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                    δ.
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Best Local
                                               Matches
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08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-
03-SEP-
03-SEP-
                                                                                                                                                                                                                                                                                                                                                                                 New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes -
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27-AUG-
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08-JUL-1999
                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 310-311; 1246pp; English.
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                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                 AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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 199
                        48
            AGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107
ADSSNKGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVP
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                                                           Similarity
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                                                                                               272
                                               Conservative
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                                                         25.9%;
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                                               15;
                                             Score 159.5; DB 22;
Pred. No. 1.4e-07;
5; Mismatches 26;
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RESULT 19
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                                      RESULT 20
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                                                                                                                                                                                                                                                                                                                       This invention describes the isolation of a pyruvate carboxylase from Corynebacterium glutamicum which is used in a novel method for production of lysine, threonine, homoserine, glutamate and/or arginine, variously useful as feed additives, condiments, pharmaceuticals and intermediates for fine chemicals. Increasing pyruvate carboxylase activity increases the yield of microbial production of amino acids of the asparate and/or glutamate families, e.g. about 50% more lysine, of the asparate and/or glutamate families, e.g. about 50% more lysine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Increasing increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arginine production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. glutamicum pyruvate carboxylase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW93971 standard; Protein; 1140 AA.
AAG90511;
                          AAG90511 standard;
                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-245521/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE19831609-A1
                                                                                                                                                                                                                                                                                                culture medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 11-15; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eikmanns B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyruvate carboxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KERJ ) FORSCHUNGSZENTRUM JUELICH
                                                                                                                         108
                                                                                                                                                                                                                                                                                                              10% more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 ERDAVQGGQGLIKI 121
|:|| :: :
258 AATKVEGGDLIVVV 271
                                                                                                                                                                                  48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chemical; ss.
                                                                                               AATKVEGGDLIVVV 1139
                                                                                                                        ERDAVQGGQGLIKI 121
                                                                                                                                                     ADSSNKGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVP 1125
                                                                                                                                                                                  AGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107
                                                                                                                                                                                                              32; Conser
                                                                                                                                                                                                                                                                                                             sparate and/or glutamate families, e.g. about 50% more ly:
threonine and 150% more homoserine are secreted into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microbial production activity or expression
                                                                                                                                                                                                                                                                   1140 AA;
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peters-Wendisch P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97DE-1043894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98DE-1031609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glutamicum
                         Protein; 1140 AA.
                                                                                                                                                                                                                          25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; amino acid production; lysine production; homoserine production; glutamate production; feed additive; condiment; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roduction of specific amino acids expression of pyruvate carboxylas
                                                                                                                                                                                                              15;
                                                                                                                                                                                                            Score 159.5; DB
Pred. No. 8.3e-07
.5; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sahm H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMBH.
                                                                                                                                                                                                              26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mino acids by carboxylase
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                      Length
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RESULT 21
AAG93249
ID AAG93
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                       1126
                                                                                                                                                                                                                                                                                                                                         sequences from the Coryneform bacterium Corynebacterium dilatamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                            26-SEP-2001
                                                                                 AAG93249 standard;
                                                                                                                                                                                                           1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                       AAG93249;
                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coryneform bacterium; amino organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum
                                                                                                                                                                                108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-2001
glutamicum
                                                                                                                                                                                                                                     48
                                                                                                                                                                                                                           AGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107
                                                                                                                                                       AATKVEGGDLIVVV 1139
                                                                                                                                                                               ERDAVQGGQGLIKI 121
                                                                                                                                                                                                       ADSSNKGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVP 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-376931/40.
DB; AAH65730.
                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KYOWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:
                                                                                                                                                                                                                                                                                                                   1140 AA;
                                                                                                                                                                                                                                                             25.9%;
ilarity 43.2%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0377484.
; 2000JP-0159162.
; 2000JP-0280988.
protein fragment mutant P458S
                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mizoguchi H, Ar
Senoh A, Ikeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAKKO KOGYO
                                                                                 Protein; 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4265; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ando
eda M,
                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                            Score 159.5; DB 22;
Pred. No. 8.3e-07;
5; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S, Hayashi M,
Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID NO: 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ochiai K,
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                       1140;
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                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                          Gaps
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AAB67129
ID AAB6
XX
AC AAB6
XX
DT 12-A
XX
COTY

AAB67129

AAB67129 standard; Protein; 1140

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12-APR-2001

(first entry)

Corynebacterium glutamicum

pyruvate carboxylase

RESULT

22

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1126

AATKVEGGDLIVVV 1139 ERDAVQGGQGLIKI 121

108

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Query Match
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        1067
                                                                                                                                                                                                                               analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a mutant protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 43; Page -; 246pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-376931/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coryneform bacterium; 
organic acid synthesi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KYOW ). KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                 48
AGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107
                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'nά
                                                                                                                                                                                                                    Patent Office.
                                                                                                                                                                            1140 AA;
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0377484.
2000JP-0159162.
2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mizoguchi H, Ando
Senoh A, Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "wild-type Pro substituted
                                                                                                             25.9%;
43.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Listing;
                                                                                       15;
                                                                                                         Score 159.5; DB
Pred. No. 8.3e-07
                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S, Hayashi M,
Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutein
                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ochiai
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                                                                                       Indels
                                                                                                                             Length
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                                                                                                                                 1140;
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RESULT 23
AAU98053
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                                                                                                                                                                                                           .1126 AATKVEGGDLIVVV 1139
                                                                                                 Feedback-resistant;
aspartic acid feedb
                                                                                                                                                                                                                                          1067
                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of the Corynebacterium glutamicum pyruvate carboxylase protein. This is an enzyme in the anaplerotic pathway. It can be used in the replenishment of considerate consumed during lysine and glutamic acid production in
                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium wild-type feedback-resistant pyruvate carboxylase enzyme
                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Column 31-36; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6171833-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyruvate carboxylase; anaplerotic pathway; industrial fermentation; oxaloacetate.
                                                     18-APR-2002
                                                                    WO200231158-A2
                                                                                                                                                      AAU98053;
                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acid encoding pyruvate carboxylase from Corynebacterium glutamicum, for replenishing oxaloacetate consumed during lysine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum
       (ARCH ) ARCHER-DANIELS MIDLAND CO
                      13-OCT-2000; 2000US-239913P
                                      12-OCT-2001;
                                                                                  Corynebacterium
                                                                                                                                        27-AUG-2002
                                                                                                                                                                      AAU98053 standard; Protein; 1140
                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                     industrial fermentation
                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MASI ) MASSACHUSETTS INST TECHNOLOGY
                                                                                                                                                                                                                          108
                                                                                                                                                                                                                                                         48
                                                                                                                                                                                                                                                                               Госат
                                                                                                                                                                                                                                        AGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                2001-122330/13.
DB; AAF32165.
                                                                                                                                                                                                                          ERDAVQGGQGLIKI
                                                                                                                                                                                                                                                                        Similarity
32; Conserv
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                                                                                                                                                                                                                                                                                                      1140
                                                                                                                                                                                                                                                                        Conservative
                                      2001WO-US31893
                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Lessard
                                                                                                 stant; pyruvate carboxylase; feedback inhibition resista
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                                                                                 glutamicum
                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                              25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      PA,
                                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                                                                                                                                                                                                      Willis LB;
                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                       Score 159.5; DB 2
Pred. No. 8.3e-07;
.5; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                 industrial fermentations
                                                                                                  resistant
                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                      Length 1140;
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                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                          strain, where the homologous recombination in the above steps, occurs between the host cell and the vector. The feedback resistant pyruvate carboxylase enzyme is resistant to feedback inhibition from aspartic acid. The present amino acid sequence represents the wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a new mutated, feedback-resistant pyruvate carboxylase enzyme. The invention is useful for producing an amino acid (e.g. L-Lys, L-Thr, L-Met, L-Tle, L-Glu, L-Arg and L-Pro), by culturing a host cell in a suitable media and separating the amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel mutated, feedback resistant pyruvate carboxylase enzyme polypeptide, useful for producing amino acids e.g. L-lysine, L-threonine, L-glycine, L-glutamic acid, L-proline and L-methionine and
                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                  recombination strain, and replacing the selectable marker gene in the first recombinant strain, with feedback resistant pyruvate carboxylase gene through homologous recombination to form a second recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resistant pyruvate carboxylase gene, in a Corynebacterium glutamicum, by replacing a genomic copy of the wild-type pyruvate carboxylase gene with a selectable marker gene through homologous recombination to form a firs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by culturing a host cell in a suitable media and separating the acid from the medium. The vector of the invention is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replacement of a wild-type pyruvate carboxylase gene, with a feedback
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanke
                                                                                                                                                                                                           feedback-resistant pyruvate carboxylase enzyme
                                            Local
             l Similarity 43.2
32; Conservative
                                                                                                                                                1140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; 42pp; English.
                                  25.9%;
             15;
   Score 159.5; I
Pred. No. 8.3e
15; Mismatches
e 159.5; Db 22,
1. No. 8.3e-07;
                                                                                                                                                                                                           of the invention
             Indels
                                                                    Length 1140,
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RESULT 24
AAB01436
                                            (SINS/)
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                                                                                                                                                                                                                                                   Pyruvate carboxylase; expression; amino acid biosynthesis; lysine; glutamic acid; oxaloacetate; fermentation; biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1067
                                                                                                                                                                                                                                                                                                     Pyruvate
                                                                                                                                                                                                                                                                                                                                                                                                 AAB01436 standard; Protein; 1141 AA
Sinskey
                                                                                            23-DEC-1998;
                                                                                                                          23-DEC-1998;
                                                                                                                                                        06-JUL-2000.
                                                                                                                                                                                       WO200039305-A1
                                                                                                                                                                                                                       Corynebacterium
                                                                                                                                                                                                                                                                                                                                  20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                   AAB01436;
                               (WILL/)
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                          ) SINSKEY A J.
) LESSARD P A.
) WILLIS L B.
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                                                                                                                                                                                                                                                                                                   carboxylase of C.
Lessard
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                                                                                                                                                                                                                       glutamicum
PA,
Willis LB
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RESULT 25
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Best I
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    The present invention relates to nucleic acids (AAH90701-AAH90918) denocing polypeptides (AAM01002-AAM01114), which are essential for the viability of a bacterial cell wall. The acronym CFE stands for "CEC For Expression", where CEG stands for "Conserved Essential Gene". The nucle
                                                                                                                               Claim
                                                                                                                                                                       Nucleic acids encoding conserved essential genes involved replication which are potential targets for the treatment resistant bacterial infections -
  viability of a bact
Expression", where
                                                                                                                                                                                                                                                                                                                                              Dougherty TJ,
Thanassi JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CFE; CEG; Conserved Essential Gene; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1127
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                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200149721-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antisense therapy; antibiotic
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                                                                                                                                                                                                                                                                                                                                                                                                                  (BRIM ) BRISTOL-MYERS SQUIBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM01086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM01086 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             industrial fermentations and for replenishing oxaloacetare confor biosynthesis during growth. By incorporating the pyruvate carboxylase gene in expression vectors levels of expression cap - 20 fold higher than in Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotides encoding Corynebacterium glutamicum pyruvate carboxylase useful for industrial fermentation processes comprises specific nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The
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DB; AAH90785.
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DB; AAA47533.
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                                                                                                                          Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        te carboxylase of Corynebacterium glutamicum can be used ing amino acids, preferably lysine and glutamic acid in fermentations and for replenishing oxaloacetate consumed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1141
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                                                                                                                                                                                                                                                                                                                                                                  Dougherty
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Pred. No. 8.3e
15; Mismatches
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"Conserved
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No. 8.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                  Davison DB,
  Essential
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                                                                                                                                                                                             bacterial antibiotic
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The
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nucleic
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an operon, by integrating an exogeneous nucleotide sequence comprising a portion of an open reading frame of the genomic sequence of interest (comprising 200-500 base pairs) into the genomic sequence of interest which confers a selectable phenotype to the cell, and determining cell viability with a selection agent such as chloramphenicol. The nucleic acids and proteins are also useful as vaccines and for treating bacterial infections with gene therapy and antisense therapy. The nucleic acids also enable identification of targets suitable for the treatment of
                                                                                                  Streptococcus pneumoniae proteins and screening compounds for antibacterial
                                                                                                                                                                                                                                                                                                                                                                             Treatment; bacterial;

 pneumoniae

                                                                                                                                           N-PSDB; AAZ96245
                                                                                                                                                                                 Stodola RK;
                                                                                                                                                                                               Black MT,
                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                               16-AUG-1996;
                                                                                                                                                                                                                                                                         15-AUG-1997;
                                                                                                                                                                                                                                                                                                   19-FEB-1998
                                                                                                                                                                                                                                                                                                                           WO9806734-A1
                                                                                                                                                                                                                                                                                                                                                    Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY85871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY85871 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             determining whether a genomic nucleotide sequence of interest is essential for viability of a bacterial cell or whether it resides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acids are useful for detecting the presence of proteins essential viability of a bacterial cell wall in samples such as cells, tissue biological fluids, blood, serum, nose, ear or throat swabs with light and for detecting corresponding target nucleic acid molecules with complementary sequences. The nucleic acids are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 NEIPAPKDGVVTEILVSNEEMVEFGKGLVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 PAPAE----ASVASEGNLVESPLVGVVYLAAGPDKPAFVTVGDSVKKGQTLVIIEAMKVM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 PAPAAGGAGAGKAGEGE-IPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKME
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                                                                                                                                                                                             Hodgson
                                                                                                                                                                                                                                                                                                                                                                           prevention; dia
antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                resistant bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  derived protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
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                                                                                                                                                                                                                                                                                                                                                                      disease; diagnosis; gene therapy; screening;
al; antibiotic; pathogenesis; infection.
                                                                                                                                                                                             Knowles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163
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Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                   #80.
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                                                                                                               related DNA -
                                                                                                    activity
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                                                                                                                                                                                            Nicholas
                                                                                                                useful
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This invention describes novel isolated Streptococcus pneumoniae polynucleotides (see AAZ96173-Z96494) and their encoded proteins AAY85792-Y86182). The DNA, vectors and host cells described in the method of the invention are useful for the recombinant expression

the recombinant expression of the

(see

polypeptides

Claim

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Page 374; 640pp;

English.

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RESULT 27
AAU37770
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Best Local (
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       The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such a polypeptide. They can also be used to screen for compounds whice interact with and inhibit or activate such a polypeptide. The polypeptides (or DNA encoding them, via gene therapy) are also useful for inducing an immunological response in a mammal. The antagonists as useful to inhibit such bacterial polypeptides. The polypeptides are particularly useful to identify antimicrobial compounds and antibioted. They are also useful to determine their role in pathogenesis of
                                                                                                            New polynucleotides for the identification antibiotics, comprise sequences of antisens
                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                     Example
                                                                                                                                                  N-PSDB;
                                                                                                                                                                                        Yamamoto
                                                                                                                                                                                                    Haselbeck
                                                                                                                                                                                                                                                                                                                  21-MAR-2000;
23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                          WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU37770 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection, dysfunction and disease.
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                                                                                                                                                                                                                                                                  27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                       26-MAY-2000;
                                                                                                                                                                                                                            (ELIT-)
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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Xu HH;
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Pred. No. 8.
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                                                        New polynucleotides antibiotics, compris
                                  Example 3;
                                                                                              N-PSDB;
                                                                                                                                              Haselbeck
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                  Yamamoto
                                                                                                                                                                                                          27 - NOV - 2000;
22 - DEC - 2000;
                                                                                                                                                                                                                                                                     21-MAR-2000;
                                                                                                                                                                                                                                                                                             21-MAR-2001;
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; antibacterial; drug design.
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2000US-242578P.
2000US-253625P.
2000US-257931P.
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Pred. No. 1
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The invention relates to antisense

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proliferation,

inhibitors their use

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genes essential identifying the

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RESULT 29
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                                                                                                                                                                                                                                                                                                                                      Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetowani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Mg E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-García P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                               Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2001; 2001WO-FR01118
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Pred. No. 1.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 monocytogenes EGD-e (see ABAGGA41). The genome sequence and fragments of control of the related organisms, and for studying genetic monocytogenes and related organisms, and for studying genetic concorded by the genomes. The present sequence is a protein concorded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin control of the genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and concortogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat fits wipe, introluby miblished not sequences.
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Best Local
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                                                                                                                 21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1078 VGATMTGSVIQVVVKKGDSVKKGDPLLITEAMKMETTIQAPFDGEVSSIYVSDGDTIESG 1137
                         WPI; 2001-611495/70
                                                   Yamamoto
                                                                 Haselbeck
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                                                                                                                                                                                                                                                                                                               Staphylococcus
                                                                                                                                                                                                                                                                                                                                          antibiotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU36768 standard; Protein; 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1138 DLLIEV 1143
                                                                                         (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the
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                                                                                                                                                                                                                                                                                                                                        prokaryotic cellular
; antibacterial; drug
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                                                                                                                 2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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Pred. No. 1.5e-06;
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Search completed: May 1, 2003, 07:53:54 Job time: 43.3958 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC for homologous nucleic acids which are required for cell proliferation in CC a wide variety of organisms. The present sequence represents an CC use variety of organisms. The present sequence represents an CC in the printed specification, but was obtained in electronic CC format directly from WIPO at CC format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.4
Best Local Similarity 29.2
Matches 42; Conservative
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                                                                                                                                                  1045 DGVIKQVTVNNGDTIATGDLLIEI 1068
                                                                                                                                                                                                                                                                                         935 NGETVEIEIDKGKRLIIKLETISEPDENGNRTIYY-----AMNGQARRIYIKDEN 98
                                                                                                                                                                                                                         98
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                                                                                                                                                                                                                  DGKVEKVLVKERDAVQGGQGLIKI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1073 AA;
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AAB70157
ABB04577
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AAU23724
AAG78644
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AAY85871
AAY14927
AAU35213
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ABB73518
AAU37770
AAU38022
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AAU98052
ABP28014
AAU03126
AAU33972
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AAB79298
AAB79299
AAB83180
AAW93971
AAU34443
ABP319331
ABP31973
AAG75011
ABP41119
AAU04858
ABG11227
AAM39515
AAM439515
AAM4365021
AAR65021
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ABP34278
AAG81776
AAU98723
AAU98724
AAU98724
AAW72900
AAY21917
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ABB66605
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AAU30456
AAY37083
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AAU00511
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ABB54089
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Novel human secret protein involved i Staphylococcus aur Staphylococcus eni Synechococcus biot Synechococcus biot Synechococcus biot Human biotin-depen S. epidermidis ope S. coelicolor Acca G. coelicolor Acca Urea amide lyase. Mycobacterium tube M. tuberculosis an Anabaena biotin ca Anabaena biotin ca C glutamicum prote Corynebacterium gl Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog M. vaccae antigen
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Streptococcus pneu
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S. pneumoniae deri
Amino acid sequenc
Enterococcus faeca
Human endometrium
Novel human enzyme
CoA carboxylase 41
Human protein sequ
DNA encoding human
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Lactococcus lactis
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Bacillus subtilis Pyruvate carboxyla Corynebacterium mu Streptococcus poly Streptococcus pyog Staphylococcus aur Staphylococcus aur C. glutamicum pyrú
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C glutamicum prote
Corynebacterium gl Novel human diagno Human polypeptide Human polypeptide Biotinylation pept Corynebacterium gl Corynebacterium wi Human ovarian anti Micromonospora eve Novel mar regulate Human carboxylase-Amino acid sequenc E. coli cellular p Corynebacterium Corynebacterium Corynebacterium Listeria Human colon monocytog cancer

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RESULT 1
AAR28177
ID AAR2
                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The P.shermanii 1.3S polypeptide is a preferred avidin-binding polypeptide for inclusion in the recombinant hybrid polypeptide of the invention. In the hybrid, a polypeptide of interest is fused to the C-terminus of the avidin-binding polypeptide. The hybrid polypeptide can then be recovered in a single chromatographic step
                          Sequence
                                                                                                      Claim 6; Page 23; 40pp; English.
                                                                                                                       binding
                                                                                                                                                  WPI; 1992-367575/45
N-PSDB; AAQ29975.
                                                                                                                                                                                                                                                                        EP511747-A.
                                                                                                                                                                                                                                                                                                  Key
Region
                                           nsing
                                                                                                                                 Hybrid
                                                                                                                                                                            Cress
                                                                                                                                                                                                                      19-APR-1991;
                                                                                                                                                                                                                                        07-APR-1992;
                                                                                                                                                                                                                                                          04-NOV-1992
                                                                                                                                                                                                                                                                                                                             Propionibacterium shermanii
                                                                                                                                                                                                                                                                                                                                             affinity chromatography
                                                                                                                                                                                                                                                                                                                                                      avidin-binding;
                                                                                                                                                                                                                                                                                                                                                                      1.3S polypeptide of Propionibacterium shermanii
                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                          AAR28177;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR28177 standard; Protein; 123
                                                                                                                                                                                            (ROHM ) ROHM - 6-HAAS CO.
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108
104.5
                                                                                                                                                                            DE,
                                           avidin monomer affinity chromatography.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10,
                                                                                                                       polypeptide - contains a polypeptide fused to an
g polypeptide contg. a biotin attachment domain
                                                                                                                                                                            Haase FC
                           123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                      91US-0687819
                                                                                                                                                                                                                                        92EP-0303067
                                                                                                                                                                                                                                                                                        Location/Qualifiers
58..100
/label= biotin-binding_recognition_sequence
                                                                                                                                                                                                                                                                                                                                                     biotin; protein purification;
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1835
613
155
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100.
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AAG46635
AAR42839
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AAG17820
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AAG46637
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AAG81854
ABP38749
Score
Pred.
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342; DB 13;
No. 5.4e-34;
         Length 123;
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Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
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Expressed antigen 
Expressed antigen
                                                                                                                                avidin
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Antigen 1 from clu
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RESULT 3
AAY78908
ID AAY7

AAY78908 standard;

Protein;

194

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FIR XXX

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AAY84002
ID AAY8
XX
AC AAY8
XX
AC AAY8
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DT 03-C
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DE Amir
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     VISEMARE 2000
                                                                                                                                                     The present sequence represents a Treponema pallidum protein, which used to produce a fusion protein antigen for use in the method of the invention. The specification describes a method for detecting antibodies against Treponema pallidum. The antibodies are detected in a sample by reaction with a fusion protein antigen, present in the mixture in limiting concentration. The fusion protein antigen comprises a Treponema pallidum membrane antigen. The method is used for diagnosis of syphilis.
                                                                                                                                                                                                                                                                               Immunoassay for anti-Treponema pallidum antibodies, used for diagnosis of syphilis using a fusion protein of membrane antigen with peptide sequence that can be biotinylated in vivo -
                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                   Sequence
                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                               Mullenix MC,
                                                                                                                                                                                                                                                                                                                                                                                                           04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                12-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PinPoint vector; fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY84002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY84002 standard;
                                                                                                                                                                                                                                                                                                                                                                                   (BECT ) BECTON DICKINSON &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence
 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114
                     61
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                                                      EGEIPAPLAGTVSKITVKEGÖTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
                  QGGQGLIKIG 70
                                                                                                                                                                                                                                                                                                                                         2000-226057/20
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QGGQGLIKIG
                                          EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV
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                                                                                                                                   126
                                                                                       Conservative
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122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                100.0%;
                                                                                                                                                                                                                                                           16pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein antigen; membrane antigen; syphilis.
                                                                                                                                                                                                                                                                                                                                                                                     ဗ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126
                                                                                       0;
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                                                                                                 Score 342;
Pred. No. 5.
                                                                                                                                                                                                                                                           English.
                                                                                       Mismatches
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                                                                                     DB 217)
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                                                                                                            Length
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                                                                                                            126;
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RESULT 4
AAW11886
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Best Local
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                                                                                                                                                                                                                                                                             including humans. The OspC nucleotide sequence provides a superior diagnostic antigen that detects early Lyme disease infection, predicts successful eradication or the organism from the host, and discriminates between individuals with Lyme disease and individuals who have been vaccinated with an OspA Lyme disease vaccination. Detection of anti-Ospa borreliacidal antibodies advantageously gives an early diagnosis which anti-OspA and anti-OspA borreliacidal antibodies advantageously gives and carry diagnosis which canti-OspA and anti-OspA borreliacidal antibodies cannot do. Unlike vaccination with OspA, vaccination with OspC results in clearance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunogenic polypeptides useful as a vaccine against Lyme disease and for treating and detecting borrelia infection in mammals consists an epitope of Borrelia burgdorferi OspC fragment -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78908
                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the Borrelia burgdorferi outer surface protein (OspC) DraI fragment amino acid sequence. The polypeptide contains an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Callister SN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer surface protein C (OspC) DraI fragment amino acid sequence
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Fig 4; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-FEB-2000
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           AAW11886;
                                 AAW11886 standard; protein;
                                                                                                                                                                                                                                                                     spirochetes and resolution of symptoms even
                                                                                                                                                                                                                                                                                                                                                                          is used to prevent (via vaccination), treat or detect Borrel (especially B. burgdorferi) infections, i.e. Lyme disease, i
                                                                                                                                                                                                                                                                                                                                                                                                  diagnose B. borrelia infection in mammals. The OspC
                                                                                                                                                                                                                                                                                                                                                                                                            rapidly synthesised by B. burgdorferi shortly after attachment infected ticks to mammalian hosts. The OspC protein sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                    (OspC) DraI fragment amino acid sequence. The polypeptide contains an immunological epitope used in the invention. Large amounts of OspC are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GUND-) GUNDERSEN LUTHERAN MEDICAL FOUND INC
                                                                                           113
                                                                                                                 61
                                                                                                                                        53
                                                                                         1 QGGQGLIKIG 70
|||||||||
3 QGGQGLIKIG 122
                                                                                                                                                   EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-195305/17.
                                                                                                                                       EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 112
                                                                                                                                                                                      70;
                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                           with
                                                                                                                                                                                                                                   194 AA;
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                         B. burgdorferi
                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; OspC; immunological epitope; Lyme disease;
Borrelia infection; diagnose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SD,
                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schell RF,
                                                                                                                                                                                   Score 342; DB 21;
Pred. No. 9.7e-34;
; Mismatches 0;
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                                                                                                                                                                                                            DB 21;
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                                                                                                                                                                                                                                                                     administered after
                                                                                                                                                                                                         Length
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                             sequence is used to
                                                                                                                                                                                                            194;
                                                                                                                                                                                                                                                                                                                                                                           in mammals
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                                                                                                                                                                                                                                                                                                                  anti-OspC
                                                                                                                                                                                   Gaps
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RESULT 5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hantavirus antigen protein and monoclonal antibody - used diagnosis and treatment of hantavirus infection {f T}
 04-SEP-1998;
                                                                                                   EP985931-A2
                                                                                                                                  Synthetic.
Treponema pallidum.
                                                                                                                                                                                                                                                       03-JUL-2000
                                                                                                                                                                                                                                                                                         AAY84001;
                                                                                                                                                                                                                                                                                                                       AAY84001 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              their specificity to Hantavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 17; 18pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-083468/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hantavirus nuclear protein; antigen; monoclonal antibody,
diagnosis; specificity.
                                                                   15-MAR-2000
                                                                                                                                                                                    PinPoint vector;
                                                                                                                                                                                                                      Amino acid sequence of a T. pallidum fusion protein antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ATAT-) A & T KK.
(ARIK/) ARIKAWA J.
(HASH/) HASHIMOTO N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-1995;
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                                 12-AUG-1999;
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98US-0148920.
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                                                                                                                                                                                    fusion protein antigen; membrane antigen; syphilis
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Pred. No. 1.4e-33;
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(BECT) BECTON DICKINSON & CO

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RESULT 6
AAY84003
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Best Local
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Claim 9; Page 14-15; 16pp; English.
                                     Immunoassay for anti-Treponema pallidum antibodies, used for diagno of syphilis using a fusion protein of membrane antigen with peptide sequence that can be biotinylated in vivo -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a Treponema pallidum fusion protein antigen. The protein is used in the method of the invention. The specification describes a method for detecting antibodies against Treponema pallidum. The antibodies are detected in a sample by reaction with a fusion protein antigen, present in the mixture in limiting concentration. The fusion protein antigen comprises a Treponema pallidum membrane antigen. The method is used for diagnon the protein protein pallidum membrane antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoassay for anti-Treponema pallidum antibodies, used for diagnosis of syphilis using a fusion protein of membrane antigen with peptide sequence that can be biotinylated in vivo
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                                                                                                                                                                       Mullenix MC,
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                                                                                                                                                                                                                                                                                                                                                                                                 Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                  PinPoint vector; fusion protein antigen; membrane antigen; syphilis
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Pred. No. 1.4e-33;
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Best Local 9
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02-JUN-2000;
07-JUL-2000;
polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the method of the invention. The special form of detecting antibodies against Treponema pallidum. The antibodies are detected in a sample by reaction with a fusion protein antigen, present in the mixture in limiting concentration. The fusion protein antigen comprises a Treponema pallidum membrane antigen. The method used for diagnosis of syphilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                     Claim 6;
                                                                                                                                                                            Propionibacterium acnes vaccinating against and treating acne vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                  SEQ ID No 12317; 1069pp;
                                                                                                                           AAU39105-AAU68017 represent Propionibacterium acnes
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; 2000US-208841P.
; 2000US-216747P.
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e J, Zha
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                   The present invention relates to the genomic sequence of Pyrococcus abyssi (see AARB6431 and AAH41223-7) and P. abyssi proteins. P. abyssi a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up 110 degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143,
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Weissenbach J,
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ed. No. 2.4e-24;
Mismatches 11;
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                  The present invention relates to a new mutated, feedback-resistant pyruvate carboxylase enzyme. The invention is useful for producing an amino acid (e.g. L-Lys, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro), by culturing a host cell in a suitable media and separating the amino acid from the medium. The vector of the invention is useful for replacement of a wild-type pyruvate carboxylase gene, with a feedback
                                                                                                                     Novel mutated, feedback resistant pyruvate carboxylase enzyme polypeptide, useful for producing amino acids e.g. L-lysine, L-threonine, L-glycine, L-glutamic acid, L-proline and L-meth
 resistant
replacing
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                                                                       The present invention relates to
                                                                                          Claim 17; Fig 1; 42pp;
                                                                                                                L-isoleucine
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acid feedback inhibition resista
 pyruvate
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Best Local Similarity
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                                                                         , Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a selectable marker gene through homologous recombination to form a first recombination strain, and replacing the selectable marker gene in the first recombinant strain, with feedback resistant pyruvate carboxylase gene through homologous recombination to form a second recombinant strain, where the homologous recombination in the above steps, occurs between the host cell and the vector. The feedback-resistant pyruvate carboxylase enzyme is resistant to feedback inhibition from asparitic acid. The present amino acid sequence represents the feedback-resistant
                                                                                             The sequence is that of a portion of the alpha subunit of Klebsiella pneumoniae oxalacetate decarboxylase. It is used as part of a fusion protein allowing for post-translation biotination which provides a marker for the fusion protein that can be used directly or indirectly to identify the fusion protein or to isolate it from a mixt. of other materials such as host cell culture media.
                                                                                                                                                                                           Claim
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                                                                                                                                                                                                                                                                                              Cronan JE;
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18-MAY-1990;
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                                                                                                                                                                                         6; Page 57;
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J. No. 1.2e-11;
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Daniels J, Goewer
Daniels J, Goewer
Chakraborty T, Domann E, F
Chakraborty T, Baquero F, F
Chakraborty T, Baquero B, F
Chakraborty T, B
Chakraborty
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bacterial infection; disease.
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nn E. Hain T. Berche P. Cha
zro F. Garcia Del Portillo F.
os B. Wehland J. Kaerst U,
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Entian K, Hauf
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Genomic sequence for Listeria monocytogenes, useful and prevention of Listeria and related bacterial in related polypeptides infections,

Claim 6; SEQ ID No 317; 192pp; French.

B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the prints specification, but was obtained in electronic format directly from WIPP at fire wipo.int/pub/published_pct_sequences. The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for blosynthesis and biodegradation, especially blosynthesis of Vitamin for blosynthesis and biodegradation, especially blosynthesis of Vitamin part of the printed directly from WIPO the genome by L. F g

Sequence 1146 AA

Matches

29;

Conservative

17;

20;

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Gaps

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Owery Match
Best Local Similarity

45.98;

Score 157; DB 23; Pred. No. 3.8e-10; Mismatches

Length 1146; Indels

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RESULT 12
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08-JUL-1999;
09-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis; Corynebacterium diphtheriae; evolutionary study.
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                    AG.
Kroeger
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99DE-1042086.
99DE-1042087.
99DE-1042088.
                                       99DE-1042095.
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В,
Schroeder
H,
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production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleoside, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae in a subject. (I), (II) or host cells containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms related to in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a colity of a suppression of sugars, and in modulating high-energy molecule production in a colity of a suppression of sugars, and in modulating high-energy molecule production in a colity of a suppression of sugars, and in modulating high-energy molecule production in a colity of the suppression of sugars, and in modulating high-energy molecule production in the suppression of the suppression of sugars, and in modulating high-energy molecule production in the suppression of the suppression of suppression of the suppression of the suppression of the suppression of suppression of the suppression of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        energy production. The C. glutamicum SMP gene can be used in vectors
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in a cell
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DB; AAF71415.
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(i.e.
NADPH).
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Best Loc Matches Query Match госат _ EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60 Similarity Conservative 45.5%; 14; Score 155.5; DB 22; Pred. No. 9e-11; 4; Mismatches 23; Indels Length 1; Gaps ۲,

262

Sequence

272 AA;

Qγ 밁 263 61 EGGDLIVVV 271 QGGQGLIKI 69 밁 δã

RESULT 13 AAB79299 Corynebacterium glutamicum SMP protein sequence SEQ ID NO:114. 30-APR-2001 AAB79299 standard; Protein; 272 (first entry)

Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme diagnosis; Corynebacterium diphtheriae; evolutionary study.

Corynebacterium glutamicum.

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23-JUN-2000; 2000WO-IB00943

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08-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                    acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae in a subject. (I), (II), (II) or host cells containing them are used to map genomes of organisms related to C. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
                                                                                                                                                                                                                                                                                                                                               metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrindidine base, and cleaning and a purine or production of the chemicals, such as, an organic acid, a production of the chemicals, such as, an organic acid, a production of the chemicals, such as, an organic acid, a production of the chemicals, such as, an organic acid, a production of the chemicals, such as, an organic acid, a production of the chemicals, such as, an organic acid, a production of the chemicals, such as a contract of the chemicals.
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03-SEP-1999;
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27-AUG-1999
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                                  204
   61 QGGQGLIKI 69
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                                              KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVPAATKV
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DB; AAF71416.
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99DE-1040765.
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                                                                                              14;
                                                                                          Score 155.5; DB Pred. No. 9e-11; 4; Mismatches
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Matches 30
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                                         AAW93971 standard; Protein; 1140 AA
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01-NOV-1999; 99JP-0311147
21-APR-2000; 2000JP-0120687
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pdhA; pc; ppc; acn; icd;
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DB; AAF87437.
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                                                                                                                                                                       EGGDLIVVV
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                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 132-135; 215pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nonaka G,
Matsui K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1139 AA;
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                       1138
                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                          45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsuzaki Y,
Kawahara Y, F
                                                                                                                                                                                                                                                                                                                                                                   15;
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                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Akiyoshi N,
Kurahashi O,
                                                                                                                                                                                                                                                                                                                                                                                             No. 5.8
                                                                                                                                                                                                                                                                                                                                                                                             .8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                    BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   production
                                                                                                                                                                                                                                                                                                                                                                                                                    22;
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Nakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of L-amino
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30-JUN-1999

(first

entry)

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RESULT 16
AAG90511
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Best Local
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N-PSDB; AAX24102.
                                                                                  C glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                 intermediates for fine chemicals. Increasing pyruvate carboxylase activity increases the yield of microbial production of amino acids of the asparate and/or glutamate families, e.g. about 50% more lysine, 40% more threonine and 150% more homoserine are secreted into the
                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes the isolation of a pyruvate carboxylase from Corynebacterium glutamicum which is used in a novel method for production of lysine, threonine, homoserine, glutamate and/or arginine, variously useful as feed additives, condiments, pharmaceuticals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE19831609-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arginine production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. glutamicum
                                              Coryneform bacterium; organic acid synthesi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      threonine production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyruvate carboxylase;
                        Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Increasing microbial production of specific amino acids by increasing activity or expression of pyruvate carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KERJ ) FORSCHUNGSZENTRUM JUELICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fine chemical;
                                                                                                          26-SEP-2001
                                                                                                                                  AAG90511;
                                                                                                                                                         AAG90511 standard; Protein; 1140
                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                              1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
                                                                                                                                                                                                                                           QGGQGLIKI
                                                                                                                                                                                                                                                                KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVPAATKV 1130
                                                                                                                                                                                                                    EGGDLIVVV 1139
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 11-15; 18pp;
                                                                                                                                                                                                                                                                                                                                                                  1140 AA;
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                  protein fragment SEQ ID NO: 4265.
                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peters-Wendisch P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pyruvate carboxylase protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97DE-1043894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98DE-1031609
                      glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e; amino acid pro
n; homoserine pro
; feed additive;
                                                                                                                                                                                                                                                                                                                             44.98;
                                                          amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              German.
                                                          acid
                                                                                                                                                                                                                                                                                                                            Score 155.5; DB 2
Pred. No. 5.8e-10;
                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sahm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          production; lysine production;
production; glutamate producti
ve; condiment; pharmaceutical;
                                                          synthesis; vitamin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ξ
                                                                                                                                                                                                                                                                                                                                       DB 20;
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                                                                                                                                                                                                                                                                                                                                       Length 1140
                                                          saccharide;
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RESULT 17
AAG93249
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Best Local
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteriam are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                      1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakagawa
Tateishi
                                                                                                                                         C glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutation point of a gene, measuring expression expression profile or pattern of a gene and ide
                                                                                                    organic
                                                                                                                  Coryneform
                                                                                                                                                                                                                                                                                                                                     in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polynucleotides derived from Coryneform bacteria, mutation point of a gene, measuring expression of a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAH65730
                         Misc-difference
                                                               Synthetic
                                                                            Corynebacterium
                                                                                                                                                                    26-SEP-2001
                                                                                                                                                                                              AAG93249;
                                                                                                                                                                                                                      AAG93249
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide an sequences from the Coryneform bacterium Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European
                                                                                                                                                                                                                                                                                                              61 QGGQGLIKI 69
                                                                                                                                                                                                                                                                                                                                                      1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
                                                                                                                                                                                                                                                                                      EGGDLIVVV 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-376931/40
                                                                                                                                                                                                                                                                                                                                                                                          31;
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                      standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:
                                                                                                                bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1140 AA;
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2000JP-0159162.
2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mizoguchi
Senoh A,
                                                                                                    synthesis; mutant;
                                                                                                                                         protein
                                                                                                                                                                  (first entry)
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                        Location/Qualifiers
                                                                          glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                     45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4265;
                                                                                                                                         fragment mutant P458S
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Ikeda M,
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                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                       1140
                                                                                                                                                                                                                                                                                                                                                                                         Score 155.5; DB 2
Pred. No. 5.8e-10;
1; Mismatches 23
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Ozaki A;
                                                                                                     mutein
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ion of a gene, analysing
identifying homologous
                                                                                                                                                                                                                                                                                                                                                                                          23;
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                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1140;
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/note= "wild-type Pro substituted by

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RESULT 18
AAB67129
ID AAB67
XX AAB67
AC AAB67
AC AAB67
AC ACCORY
DF 12-AP
CORY
DX CORY
CX PYRUV
KW OXALC
XX OXALC
XX OXALC
XX OXSL
PN US617
XX 09-JP
XX 09-JP
XX 03-D3-
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Matches
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07-APR-2000;
03-AUG-2000;
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                                                         US6171833-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a mutant protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakagawa
Tateishi
 23-DEC-1998;
                             09-JAN-2001.
                                                                                                               oxaloacetate.
                                                                                                                                                     Corynebacterium glutamicum pyruvate carboxylase.
                                                                                                                                                                                      12-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. The sequence is not identifying the mutation point of a gene derived from a mutation of a gene derived from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                  Corynebacterium
                                                                                                                         Pyruvate carboxylase;
                                                                                                                                                                                                                AAB67129;
                                                                                                                                                                                                                                        AAB67129 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 43; Page -; 246pp +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2000; 2000EP-0127688
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                EGGDLIVVV 1139
                                                                                                                                                                                                                                                                                                                                                                                     EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
                                                                                                                                                                                                                                                                                                                                          QGGQGLIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n.
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                                                                                                                                                                                                                                                                                                                                                                                                                         45.5%;
llarity 44.9%;
Conservative 1
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; 2000JP-0159162.
; 2000JP-0280988.
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Senoh A, Ikeda
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 98US-0220081
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                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                   entry)
                                                                                                                           anaplerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for this patent did not form btained in electronic format
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eda M,
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 155.5; DB 22
Pred. No. 5.8e-10;
4; Mismatches 23;
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Ozaki A;
                                                                                                                                                                                                                                           ያ
                                                                                                                         pathway; industrial fermentation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        part of the print directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1140
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RESULT 19
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Best Local
                                 Novel mutated, feedback resistant pyruvate carboxylase enzyme polypeptide, useful for producing amino acids e.g. L-lysine, L-threonine, L-glycine, L-glutamic acid, L-proline and L-methionine L-isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1131
                                                                                                                                                                                                                                                                                                                                 Corynebacterium wild-type feedback-resistant pyruvate carboxylase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1072 KGHVAAPEAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVPAATKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum pyruvate carboxylase protein. This is an enzyme in the anaplerotic pathway. It can be used in the replenishment oxaloacetate consumed during lysine and glutamic acid production in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid encoding pyruvate carboxylase from Corynebacterium glutamicum, for replenishing oxaloacetate consumed during lysine and glutamic acid production in industrial fermentations -
                                                                                                                                                                                                                                                                          Corynebacterium
                                                                                                                                                (ARCH ) ARCHER-DANIELS MIDLAND
                                                                                                                                                                         13-OCT-2000; 2000US-239913P
                                                                                                                                                                                                12-OCT-2001;
                                                                                                                                                                                                                          18-APR-2002
                                                                                                                                                                                                                                                 WO200231158-A2
                                                                                                                                                                                                                                                                                                  aspartic acid
                                                                                                                                                                                                                                                                                                             Feedback-resistant;
                                                                                                                                                                                                                                                                                                                                                               27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                            AAU98053 standard; Protein; 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Column 31-36; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAF32165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sinskey AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MASI ) MASSACHUSETTS INST TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     industrial fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
                                                                                                2002-463267/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGGDLIVVV 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGGQGLIKI
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                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 45.5%;
1 Similarity 44.9%;
31; Conservative 1
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                                                                                                                                                                                                2001WO-US31893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lessard
                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                  stant; pyruvate carboxylase; enzyme;
feedback inhibition resistant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0220081
                                                                                                                                                                                                                                                                         glutamicum
                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PΑ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Willis LB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 155.5; DB 22,
Pred. No. 5.8e-10;
4; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1130
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Disclosure;

Fig

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42pp; English

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RESULT 20
AABO1436
ID AABO1
XX AABO1
XX 20-OC
XX 20-OC
XX PYTUV
KW 91uta
XX WO200
XX WO200
XX WO200
XX WO200
XX WO21
PD 06-JU
XX 23-DE
XX (SINS
PA (LESS
PA (WILL
XX WPI;
DR WPI;
CT Novel
PT Carbo
PT Carbo
CC The I
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Best Local S
Matches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyruvate
glutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid (e.g. L-Lys L-Thr. L-Met, L-ILe, L-Glu, L-Arg and L-Pro), by culturing a host cell in a suitable media and separating the amino acid from the medium. The vector of the invention is useful for replacement of a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate carboxylase gene, in a Corynebacterium glutamicum, by replacing a genomic copy of the wild-type pyruvate carboxylase gene with a selectable marker gene through homologous recombination to form a first recombination strain, and replacing the selectable marker gene in the first recombination strain, with feedback resistant pyruvate carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene through homologous recombination to form a second recombinant strain, where the homologous recombination in the above steps, occurs between the host cell and the vector. The feedback-resistant pyruvate carboxylase enzyme is resistant to feedback inhibition from aspartic acid. The present amino acid sequence represents the wild-type feedback-resistant pyruvate carboxylase enzyme of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates
                                                                                              Novel polynucleotides encoding Corynebacterium glutamicum carboxylase useful for industrial fermentation processes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pyruvate carboxylase enzyme. amino acid (e.g. L-Lys, L-Th
                                                Claim 3;
                                                                                specific
                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                  Sinskey AJ,
                                                                                                                                                                                                                               (SINS/) SINSKEY A J.
(LESS/) LESSARD P A.
(WILL/) WILLIS L B.
                                                                                                                                                                                                                                                                                                   23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                  23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                    06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                   WO200039305-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyruvate carboxylase of C. glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB01436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB01436 standard; Protein; 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVPAATKV 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGGQGLIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
                                                                                                                                                2000-465746/40
DB; AAA47533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGGDLIVVV 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                              Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carboxylase; expression; amino acid biosynthesis; lysine; acid; oxaloacetate; fermentation; biosynthesis.
                                                                                nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                  Lessard
                                              1; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                   98WO-US27301.
                                                                                                                                                                                                                                                                                                                                   98WO-US27301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.5%;
                                                                                                                                                                                                  PA,
                                                                                                                                                                                                  Willis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 155.5; DB 23;
Pred. No. 5.8e-10;
14; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s to a new mutated, feedback-resistant
The invention is useful for producing
r, L-Met, L-Ile, L-Glu, L-Arg and L-Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for producing an
L-Arg and L-Pro),
                                                                                              um pyruvate
comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;;
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pyruvate carboxylase of Corynebacterium glutamicum oproducing amino acids, preferably lysine and glutami

can

be

L-lysine, and L-methionine

and

used d in

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RESULT 21
AAU98052
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Best Local S
Matches 31
       Novel mutated, feedback polypeptide, useful for L-threonine, L-glycine, L-isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1132 EGGDLIVVV 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1073 KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVPAATKV 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    industrial fermentations and for replenishing oxaloacetate consumed for biosynthesis during growth. By incorporating the pyruvate carboxylase gene in expression vectors levels of expression can be 2 - 20 fold higher than in Corynebacterium glutamicum.
                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                           Feedback-resistant; pyruvate carbo
aspartic acid feedback inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU98052 standard; Protein; 1140
                                                           WPI; 2002-463267/49.
                                                                                Hanke
                                                                                                                        13-OCT-2000; 2000US-239913P
                                                                                                                                            12-OCT-2001;
                                                                                                                                                                 18-APR-2002
                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium mutant feedback-resistant pyruvate carboxylase enzyme:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU98052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                  (ARCH ) ARCHER-DANIELS MIDLAND
                                                                                                                                                                                    WO200231158-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGGQGLIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
                                                                                                                                                                                                                                                                                                                       /note=
182
                                                                                                                                                                                                                                                                                                   /note=
206
                                                                                                                                                                                                                                                                                                                                            /note=
153
                                                                                                                                                                                                                    /note=
1116
                                                                                                                                                                                                                                                             455
                                                                                                                                                                                                                                                                               /note=
227
                                                                                                                                                                                                                                                                                                                                                                                                       glutamicum
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                        1110..1122
                                                                                                                                                                                                                                                                     note-
                                                                                                                                                                                                                                                  note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.9%;
                                                                                                                                                                                                       "Wild-type
                                                                                                                                                                                                                                                                                                            "Wild-type Ala
                                                                                                                                                                                                                                                                                                                                                      "Wild-type Met
                                                                                                                                                                                                                                               "Wild-type
                                                                                                                                                                                                                                                                    "Wild-type His
                                                                                                                                                                                                                                                                                        "Wild-type
                                                                                                                                                                                                                                                                                                                                "Wild-type Glu
                resistant pyruvate carboxylase enzyme producing amino acids e.g. L-lysine, L-glutamic acid, L-proline and L-meth
                                                                                                                                                                                                                            "Specifically claimed in claim 18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 155.5; DB 2
Pred. No. 5.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                       carboxylase;
                                                                                                   င္ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                Ala
                                                                                                                                                                                                                                                                                        Ala
                                                                                                                                                                                                                                                                                                                                                                                                                            resistant; muta
                                                                                                                                                                                                        Asp substituted by
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                                                                                                                                                                                                                                                                                                                                                      substituted
                                                                                                                                                                                                                                                                                         substituted
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                                                                                                                                                                                                                                                                                                                                                                                                                            mutant; mutein
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                                                                                                                                                                                                        Glu"
                                                                                                                                                                                                                                                Gly'
                                                                                                                                                                                                                                                                                        Ser"
                                                                                                                                                                                                                                                                                                            Ser"
                                                                                                                                                                                                                                                                                                                                Asp"
                                                                                                                                                                                                                                                                                                                                                      Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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The present invention relates to

resent invention relates to a new mutated, feedback-resistant ate carboxylase enzyme. The invention is useful for producing acid (e.g. L-Lys, L-Thr. L-Met. L-Tle. L-Glu, L-Arg and L-Pro Luring a host cell in a suitable media and separating the amplituring a host cell in a suitable media and separating the amplitude of the contract o

L-Pro),

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Claim 1; Page

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English.

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ABP2801
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Best Local :
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                                                        Telford J, r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        resistant pyruvate carboxylase gene, in a Corynebacterium glutamicum, by replacing a genomic copy of the wild-type pyruvate carboxylase gene with a selectable marker gene through homologous recombination to form a first recombination strain, and replacing the selectable marker gene in the first recombination strain, with feedback resistant pyruvate carboxylase gene through homologous recombination to form a second recombinant strain, where the homologous recombination in the above steps, occurs between the host cell and the vector. The feedback resistant pyruvate carboxylase enzyme is resistant to feedback inhibition from aspartic feedback-resistant pyruvate acid. The present amino acid sequence represents the mutant feedback-resistant pyruvate carboxylase enzyme of the invention.

Note: The present sequence is not shown in the specification but is derived from the wild-type feedback-resistant pyruvate carboxylase enzyme (AAU98053) given in figure 2 of the specification.
                                                                                                                                                        27-OCT-2000; 2000GB-0026333; 24-NOV-2000; 2000GB-0028727; 07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                              Streptococcus; GAS; GBS; grogroup A streptococcus; Strepantiinflammatory; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1072
           N-PSDB; ABN68645
                             WPI; 2002-352536/38
                                                                                                                                                                                                                                                      02-MAY-2002
                                                                                                                                                                                                                                                                                      WC200234771-A2
                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus polypeptide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP28014 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by culturing a host cell in a suitable media and separating the amino acid from the medium. The vector of the invention is useful for replacement of a wild-type pyruvate carboxylase gene, with a feedback
                                                                                                                                                                                                                       29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP28014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                            (CHIR-) CHIRON SPA
                                                                                                           (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGGQGLIKI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGGDLIVVV 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVEGKIDRVVVPAATKV 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                           INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1140 AA;
                                                                          Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                              GBS; group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.38;
                                                                                                                                                                                                                                                                                                                                            S; group B streptococcus; Streptococcus agalactiae;
Streptococcus pyogenes; antibacterial;
ction; vaccine; meningitis; gene therapy.
                                                                          Margarit Ros YI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 151.5; DB 23; Pred. No. 1.8e-09; 15; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                               5204.
                                                                          Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1140;
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New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein - \,
                                                                                                                                                              The invention
                                                                                                                                                                              Claim 1; Page 3684; 4525pp; English.
                                                                                                                                                             relates to a protein (ABP25413-ABP30895)
                                                                                                                                                            from
                                                                                                                                                             group
                                                                                                                                                             В
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streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus/GBS (Streptococcus/GAS), given in C (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) is used to detect acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity for treatecoccus proteins. Streptococcus proteins.

Sequence 166 AA;

Length 166;

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                                                                                                                                Query Match
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                                149 LVSNEDVIEFGQGLVRI 165
23
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                                                                                      1 EGEI-PAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKV 52
                                                   LVKERDAVQGGQGLIKI
                                                                         EGDIVESPLYGVAYLAASPDKPPFVAYGDTVKKGQTLVIIEAMKVMNEVPAPCDGVITEI 148
                                                                                                                      32;
                                                                                                                                 Similarity
                                                                                                                       Conservative
                                                                                                                                44.28;
                                                    69
                                                                                                                     15;
                                                                                                                                Score 151; DB 23; Pred. No. 1.7e-10;
                                                                                                                      Mismatches
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RESULT
   Virulence; attenuated microorganism; Streptococcal infection; Gram-positive bacteria; antimicrobial; impetigo; pneumonia.
                                                                                             Streptococcus pyogenes virulence protein #8
                                                                                                                                                                                                                                                                                     AAU03126 standard; Protein; 134
                                                                                                                                                           23-OCT-2001
                                                                                                                                                           (first entry)
impetigo; pneumonia.
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Streptococcus pyogenes

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AAU03126
ID AAU0
XX AAU
AC AAU0
AC AAU0
AC AAU0
AC AAU0
CON Stre
XX V1ru
KW V1ru
KW Gram
XX W020
PN W020
XX 23-1
PR 23-1
              23-DEC-1999;
23-DEC-1999;
23-DEC-1999;
23-DEC-1999;
23-DEC-1999;
23-DEC-1999;
17-FEB-2000;
17-FEB-2000;
                                                                                                               23-DEC-1999;
23-DEC-1999;
23-DEC-1999;
                                                                                                                                                                                                   05-JUL-2001
                                                                                                                                                                                                                           WO200148208-A2
                                                                                                                                                   23-DEC-1999;
                                                                                                                                                                            22-DEC-2000; 2000WO-GB04997
99GB-0030466.
99GB-0030469.
99GB-0030472.
99GB-0030472.
99GB-0030474.
99GB-0030474.
2000GB-0003725.
2000GB-0003727.
                                                                                                                           99GB-0030464
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CC proteins #1-31. The S. pyogenes virulence genes can be used to CC produce attenuated microorganisms comprising a mutation that disrupt CC the expression of the virulence protein. The virulence genes, proteins CC or an attenuated microorganism are useful for therapeutic or diagnostic CC purposes. DNA encoding the virulence proteins, the proteins themselves, CC an attenuated microorganism or a vacchine comprising the virulence CC protein are useful for the manufacture of a medicament for use in CC the treatment or prevention of a condition associated with infection CC by Streptococcal or Gram-positive bacteria, for veterinary treatment, CC and in a screening assay for the identification of an antimicrobial CC drug. Disorders which can be treated using S. pyogenes virulence cC polynucleotide and polypeptide sequences include non-invasive infections CC and invasive infections e.g. impetigo, pharyngitis, mecrotising CC fasciltis, bacteraemia, streptococcal toxic shock syndrome (STSS), pneumonia and rheumatic fever. The virulence proteins are also useful CC in the preparation of antibodies.
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02-MAY-2000;
02-MAY-2000;
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17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide obtained from Streptococcus pyogenes useful for treating or preventing a condition associated with infection by Streptococcal or Gram-positive bacteria, preferably pneumonia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 40-41; 91pp; English.
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                                                        Staphylococcus aureus
                                                                                    Antisense; prokaryotic cellular antibiotic; antibacterial; drug
                                                                                                                                Staphylococcus aureus cellular proliferation protein #938
                                                                                                                                                               14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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27-SEP-200:
                            WO200170955-A2
                                                                                                                                                                                             AAU36768
                                                                                                                                                                                                                        AAU36768 standard; Protein; 1073 AA.
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2000GB-0003729.
2000GB-0003731.
2000GB-0003731.
2000GB-0003731.
2000GB-0003733.
2000GB-0003733.
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                                                                                                                                                              (first entry)
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Pred. No. 3.9e-10;
9; Mismatches 26;
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                                                                                    proliferation design.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Entercococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in prolliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell prolliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      essential prokaryotic cellular prolifera
Note: The sequence data for this patent
of the printed specification, but was ob
format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides for the identification and development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haselbeck R, Yamamoto RT,
                                                                                                                                                                                                                                                                                                               1003 IGAQMPGSVTEVKVSVGETVKANQPLLITEAMKMETTIQAPFDGVIKQVTVNNGDTIATG 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to antisense inhibitors of genes essential prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS54627.
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                             Antisense; prokaryotic cellular antibiotic; antibacterial; drug
                                                                                                          14-FEB-2002
                                                                                                                                                                                                                                                   1063 DLLIEI 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                           Staphylococcus aureus cellular proliferation protein #248.
                                                                                                                                         AAU33972;
                                                                                                                                                                        AAU33972 standard; Protein; 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1073
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2001US-269308P
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2000US-207727P.
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                                                                                                          (first entry)
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Xu HH;
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Pred. No. 7.8e-09;
                             proliferation protein;
design.
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Staphylococcus aureus

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AC AAY14
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23-OCT-2000;
27-NOV-2000;
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23-MAY-2000;
26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klabsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this pattent did not form part
     M. vaccae antigen GV-29 3' sequence
                                         25-OCT-1999
                                                                     AAY14912;
                                                                                                                                                                        1139
                                                                                                   AAY14912 standard;
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Seq ID No 5468; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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N-PSDB; AAS51831.
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                                                                                                                                                                                                                                                                                                                                                                                    of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001
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                                                                                                                                                                                                                              -2001;
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2000US-253625P.
2000US-257931P.
                                         (first entry)
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2001US-269308P
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Xu HH;
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3.5e-09;
les 22;
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23-DEC-1997;
23-DEC-1997;
11-JUN-1998;
17-SEP-1998;
M. vaccae proteins. The M. vaccae proteins may be employed to activate T cells and natural killer cells, to stimulate the production of cytokines, to enhance the expression of co-stimulatory molecules on dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The proteins can be expressed by standard recombinant methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins can be used for the treatment, prevention, and detection of disorders including infectious diseases, immune disorders and cancer. In particular, the compounds and methods are used for treatment of diseases of the respiratory system, such as mycobacterial infections, asthma, allergies, tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium vaccae protein; antigen; T cell activation; cytokine; dendritic cell maturation; infectious disease; immune disorder; canc respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 217; 243pp; English.
                                                                                                                                                                                                                                                                                                                   The invention provides heat-killed Mycobacterium vaccae, M. vaccae proteins. The M. vaccae proteins may be employ
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23-DEC-1997;
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97US-0996624.
97US-0997080.
97US-0997362.
98US-0095855.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watson
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                                                                                                                                                                                                                                                                                                                                                   recombinant
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RESULT 27 ABB73518 밁 밁 S S X S X E X Ş Ş Query Match Best Local S Matches 32 08-APR-2002 ABB73518; ABB73518 Sequence alopecia areata, and skin such as mycobacterial infections, asthma, allergies, tuberculosis, leprosy, sarcoidosis and lung cancers, and disorders of the skin such as psoriasis, atopic dermatitis, eczema, allergic contact dermatitis, carcinoma 37 97 TPLVVVG 64 QGLIKIG 70 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63 VDAPFASSVWKVDVAVGDRVVAGQPLLALEAMKMETVLRAPADGVVTQILVSAGHLVDPG 96 l Similarity 32; Conserv standard; and melanoma. 108 Conservative 103 (first entry) Æ Protein; 42.18; 47.88; cancers such as basal 9; Score 144; DB 20; Pred. No. 6.9e-10; 9; Mismatches 26; carcinoma, Length 108; Indels squamous 0 Gaps

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                                                                                                 Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                        treated may also include alopecia areata, and skin cancers such as basal cell carcinoma, squamous cell carcinoma and melanoma. The composition acts by inhibiting the Th2 immune response. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated with a skin disorder selected from psoriasis, atopic dermatitis and allergic contact dermatitis, which involves administering a composition containing delipidated and deglycolipidated Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting skin inflammation associated with skin disorder e.g. psoriasis, by administering composition comprising delipidated and deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae culture filtrate
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                                    Streptococcus pneumoniae
                                                           Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                          14-FEB-2002
                                                                                                                                                     AAU37770
                                                                                                                                                                            AAU37770 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccae cells or M. vaccae culture filtrate. The skin disorder to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method of inhibiting skin inflammation
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32; Conserv
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47.88;
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Pred. No. 6.9e-10;
9; Mismatches 26;
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RESULT 29
AAU38022
ID AAU38
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XX Antis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cc genes, their use in the discovery of novel antibiotics, the essential cc genes themselves and the encoded proteins. The prokaryotes used are convenient to the protein that coil, Staphylococcus aureus, Salmonella typhi, Klebsiella cc pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The cc invention is also useful for the identification of potential new targets cf for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, cc and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery cc programmes. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery compounds in prokaryotic cellular proliferation protein.

Cc Note: The sequence data for this patent did not form part cof the printed specification, but was obtained in electronic format directly from WIPO at the proposition in the present sequence is a stop introposition with the process of the printed specification, but was obtained in electronic content discovery format directly from WIPO at the proposition in the present sequence data for this patent did not form part compounds in electronic format directly from WIPO at the proposition in the present sequence data for this patent did not form part compounds in electronic format directly from WIPO at the proposition in the present did not form part compounds in electronic format directly from WIPO at the proposition in the present did not format directly from wiPO at the proposition in the present did not format directly from wiPO at the proposition in the present did not format directly from wiPO at the proposition in the present did not format directly from wiPO at the proposition in the present did not format directly from wiPO at the proposition in the proposition in the prese
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Best Local :
             Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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23-MAY-2000;
                                                                                  Streptococcus
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                                                                                                                                                                    AAU38022;
                                                                                                                                                                                                          AAU38022 standard; Protein;
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Yamamoto RT,
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22-DEC-2000;
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23-OCT-2000;
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                                                                                                                                                                                                                                                                                                                     144 LVSNEEMVEFGKGLVRI 160
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DB; AAS55629.
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| 32; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 AA;
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2000US-207727P.
2000US-242578P.
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2000US-257931P.
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Xu HH;
                                                                                pneumoniae cellular proliferation protein
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41.6%;
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                                                                                                                                                                                                               161 AA
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Pred. No. 1.2e
L5; Mismatches
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L.2e-09;
nes 22;
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RESULT 30
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23-MAY-2000;
26-MAY-2000;
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27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                     to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The intisense nucleic acids can also be used
CFE v9 protein sequence
                             02-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                            of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
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                                                              AAM01086
                                                                                           AAM01086 standard; Protein; 161 AA.
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                                                                                                                                                                                                                                                        EGE-IPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKV 52
                                                                                                                                                                    LVSNEEMVEFGKGLVRI 160
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DB; AAS55881.
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                                                                                                                                                                                                                                                                                       Similarity 41.0
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The present invention relates to nucleic acids (AAH90701-AAH90918)
CC encoding polypeptides (AAM01002-AAM0114), which are essential for the
CC viability of a bacterial cell wall. The acronym CFE stands for "CEG For
CC Expression", where CEG stands for "Conserved Essential Gene". The nucleic
carids are useful for detecting the presence of proteins essential for the
CC viability of a bacterial cell wall in samples such as cells, tissues,
CC biological fluids, blood, serum, nose, ear or throat swabs with ligands,
CC and for detecting corresponding target nucleic acid molecules with
CC complementary sequences. The nucleic acids are also useful for
CC determining whether a genomic nucleotide sequence of interest is
CC essential for viability of a bacterial cell or whether it resides within
CC an operon, by integrating an exogeneous nucleotide sequence comprising a
CC portion of an open reading frame of the genomic sequence of interest
CC (comprising 200-500 base pairs) into the genomic sequence of interest
CC which confers a selectable phenotype to the cell, and determining cell
CC viability with a selection agent such as vaccines and for treating bacterial
CC acids and proteins are also useful as vaccines and for treating bacterial
CC acids and proteins are also useful as vaccines and for treating bacterial
CC acids and proteins are also useful as vaccines and for treating bacterial
CC acids and protein acids and antisense therapy. The nucleic acids
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                                                                                                                                                                                                  antibiotic resistant bacterial infections.
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Patent No. 6464985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Compositions and Method Using the Borreliacidal TITLE OF INVENTION: Epitope(s) of Borrelia Burgdorferi Outer Surface TITLE OF INVENTION: Epitope(s) of Borrelia Burgdorferi Outer Surface TITLE OF INVENTION: Lyme Disease FILE REFERENCE: B. burgdorferi OspC CURRENT APPLICATION NUMBER: US/09/364,083 CURRENT FILING DATE: 1998-07-30 EARLIER APPLICATION NUMBER: 60/094,955 EARLIER APPLICATION NUMBER: 60/094,955 USANDER: Patentin Ver. 2.0 SOFTMARE: Patentin Ver. 2.0 SOFTMARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local Similarity
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Patent No. 6210676
                                                                                                                                                                                                        TITLE OF INVENTION: Compositions and Method Using the Borreliacidal TITLE OF INVENTION: Epitope(s) of Borrelia Burgdorferi Outer Surface TITLE OF INVENTION: Protein C (OSPC) for the Diagnosis and Prevention TITLE OF INVENTION: Lyme Disease FILE REFERENCE: B. burgdorferi OspC
                                                                       SOFTWARE:
                                                                                                            PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
                                                                                                                                                   FILE REFERENCE: B. burgdorferi OspC
CURRENT APPLICATION NUMBER: UZ/09/651,419
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/094,955
                                                                                                                                                                                                                                                                                                               APPLICANT:
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APPLICANT: Schell, Ronald F
APPLICANT: Jobe, Dean A
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                                    LENGTH: 194
TYPE: PRT
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                                                                                              PatentIn
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Schell, Ronald F
                                                                                                                                                                                                                                                                                                                                                                      Callister,
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                                                                                              Ver.
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                                                                                                                                                                                                                                                                                                                                                    Steven M
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US-07-956-700B-107
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Best Local Similarity
Matches 122; Conserv
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acid
                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: Lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5539092thrup
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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            60 LAGTYSKILVKEGDTYKAGQTYLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 119
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OPERATING SYSTEM:
SOFTWARE: ASCII-I
                                                                                                                                                                                                                                        TYPE: Amino acids
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                                                                       1 MKLKYTVNGTAYDVDVDVDKSHENPMGTILFGGGTGGAPAP-AAGGAGAGKAGEGEIPAP 59
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LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 120
                                                          MKLKVTVNGTAYDVDVDVDKSHENPMGTILFGGGTGGAPAPRAAGGAGAGKAGEGEIPAP
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                                                                                                                                                                                                                                                                                                        1-312-755-4489
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robert Haselkorn and Piotr Gornicki
VENTION: Cyanobacterial and Plant Acetyl-Coa
VENTION: Carboxylase
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.2e-56;
0; Mismatches 0;
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Pred. No. 1.7e-57;
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: Sequence 107_Application US/08476537

: Patefit No. 5756290
                                                                 Patent No.
                                                                               Sequence
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Best Local Similarity
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                                  GENERAL INFORMATION:
APPLICANT: Robert
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INFORMATION FOR SEQ ID NO:
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STREET:
CLITY: Chicago
CLITY: Illinois
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ATTORNEY/AGENT INFORMATION:
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    TITLE OF INVENTION:
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                                                                                                                                                            121 KIG 123
                                                                                                                                                                                           120 KIG 122
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REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
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                                                                                                                                                                                                                                       60 LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 119
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NVENTION: Cyanobacterial and Plant Acetyl-Coa
VENTION: Carboxylase
Robert Haselkorn and Piotr Gornicki
VENTION: Cyanobacterial and Plant Acetyl-CoA
VENTION: Carboxylase
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            ESS: Single
Linear
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IBM PC Compatible
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Pred. No. 1.2e
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1.2e-56;
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Best Local Similarity
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Patent No. 5972644 5786170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 122;
                                                                                                                                                                                                                                                                     Sequence 107,
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INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
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                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                             121 KIG 123
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REGISTRATION NUMBER: 33,268
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                                                                         COUNTRY:
                                                                                                      CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLKVTVNGTAYDVDVDVDKSHENPMGTILFGGGTGGAPAP-AAGGAGAGKAGEGEIPAP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                   ADDRESSEE:
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                                                                                       Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Arnold, White & Durkee
321 No. 5792627th Clark Street
                                                                                                                  321 No.
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                                                                                                                                                                                                                                                                    Application US/08475879
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                                                                         USA
                                                                                                                                                                                                        Robert Haselkorn and Piotr Gornicki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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                                                                                                                    ld, White & Durkee
5972644 5786170th Clark Street
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99.2%;
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Pred. No. 1.2e-56;
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US-07-687-819-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Haase, Ferdinand C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 1-312-755-448
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 597264 5786170thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: LI
                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Carrier Protein NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION
                                           CLASSIFICATION:
CLASSIFICATION:
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CLASSIFICATION:
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                                                                                                             CLASSIFICATION:
                                                                                                                           APPLICATION NUMBER: US FILING DATE: 19910520
                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Rohm and Haas Company STREET: Independence Mall West
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                            USA
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1-312-755-4489
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C07K15/26
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99.2%;
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Pred. No. 1.2e-56;
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                                                                                  SEQ ID NO 107
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                               Patent No. 6399342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.7
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE: Amino Patent No. 6072039
TITLE: from '
                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                         FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 08/475,879 PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                           APPLICANT: GORNICKI, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
                                                                                                                                                      PRIOR FILING DATE: 1992-10-02
                                                                                                                                                                         PRIOR APPLICATION NUMBER: 07/956,700
                                                                                                                                                                                                                                                                                               APPLICANT: HASELKORN, APPLICANT: GORNICKI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 215-592-2682
INFORMATION FOR SEQ ID NO:
OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Peptide
                                 ORGANISM: Artificial Sequence FEATURE:
                                                                     TYPE: PRT
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AUTHORS: Maloy, W L
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VOLUME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Propionibacterium shermanii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Driks, Jordan J. REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMINO ACID
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Zwolinski, G K
Kumar, K G
Wood, H G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Journal of Biological Chemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215-592-2478
                                                                                                                     Ver.
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99.2%;
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Pred. No. 1.2e-56;
0; Mismatches 0
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US-09-433-043B-128
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-128
 ; PURIFYING THEM
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/525,568
; ETLING DATE: 18-MAY-1990
; PRIOR APPLICATION DATA:
                                                                                                                APPLICANT: CRONAN, JOHN E.
TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
                                                                                                                                                                        Patent No. 5252466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 07/956,700
PRIOR FILING DATE: 1992-10-02
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ARCD:338US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HASELKORN, ROBERT APPLICANT: GORNICKI, PIOTR
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CURRENT FILING DATE: 1999-10-25
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLKVTVNGTAYDVDVDVDKSHENPMGTILFGGGTGGAPAP-AAGGAGAGKAGEGEIPAP
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                                                                                                                                                                                                                                                                                                                                              LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 120
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                                                                                                                                                                                                                                                                       123
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Pred. No. 5.4e-56;
0; Mismatches 1;
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Pred. No. 1.2e-56;
0; Mismatches 0;
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US-07-687-819-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CRONAN, JOHN E.
TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:1:
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Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Haase, Ferdinand C.

APPLICANT: Cress, Dean E.

APPLICANT: Cress, Dean E.

TITLE OF INVENTION: Carrier Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 354,266
FILING DATE: 19-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
                   CURRENT APPLICATION DATA:
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rohm and Haas Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 GLIKIG 122
                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPERATE: PatentIn Release #1.0,
                                                                                                                                                                          STREET: Independence CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GLIKIG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 PAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQ 116
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                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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97.0%;
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US/07/687,819
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Pred. No. 6.2e-26;
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Pred. No. 1.2e-47;
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                                       Version #1.25
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US-09-433-043B-127
RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-09-433-043B-127
; Sequence 127, Application US/09433043B
; Patent No. 6399342
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; FRAGMENT TYPE:
US-07-687-819-2
                                                                                                                                                             Matches
                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. SEQ ID NO 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: HASELKORN, ROBERT
APPLICANT: GORNICKI, PIOTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1992-10-02
NUMBER OF SEQ ID NOS: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GORNICKI, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 08/475,879 PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 07/956,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                           LENGTH: 170
                                      "145 QAGTVRGIAVKAGDAVAVGDTLMTL 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                             38 APAPAAGGAGAGKAGEG-EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96
                                                                       97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity es 45; Conserv
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REGISTRATION NUMBER: 22,029
REFERENCE/DOCKET NUMBER: 89
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CLASSIFICATION:
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CLASSIFICATION:
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                                                                    TDGKVEKVLVKERDAVQGGQGLIKI 121
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100.0%; Pr
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C07K15/26
C12P21/00
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Pred. No. 9.9e-16;
                                                                                                                                                                    Score 202.5; DB 4
Pred. No. 4.4e-14;
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                                                                                                                                                          Mismatches
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                                                                                                                                                                                  DB 4;
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US-08-476-537-106
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,; MOLECULE TYPE:
US-07-956-700B-106
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                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                Sequence 106, Application US/08476537 Patent No. 5756290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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APPLICANT: Robert Haselkorn and Piotr Gornicki
APPLICANT: OF INVENTION: Cyanobacterial and Plant Acetyl-Coa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 1-312-744-0090
TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 100
                                                                                   STREET: 32.
STREET: 111cago
CITY: Chicago
TATE: Illinois
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: LBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5539092thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:056
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,70
FILING DATE: 19921002
                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Cyanobacteri
TITLE OF INVENTION: Carboxylase
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                140 QAGTVRGIAVKAGDAVAVGDTLMTL 164
                                                                                                                                                                                                                                                                                                                                                                                                             97 TDGKVEKVLVKERDAVQGGQGLIKI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Arnold, White & Durkee STREET: 321 No. 5756290th Clark Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 APAPAAGGAGAGKAGEG-EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 321 No CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                     60610
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                                                                                                                                                                                                                                         Robert Haselkorn and Piotr Gornicki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 amino acids
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321 No. 5539092th Clark Street
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                                                                                                                                                                                                         Carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.6%; Score 200.5; 52.9%; Pred. No. 6.9
                                                                                                                                                                                                                          Cyanobacterial and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/07/956,700B
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                                                                                                                                                                                                                       Plant Acetyl-CoA
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SOFTWARE: ASCII-DOS CURRENT APPLICATION DATA:

APPLICATION NUMBER:

US/08/476,537

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US-08-485-607-106
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Best Local Similarity
Matches 45; Conserva
                                                                                                                                                                                                                                         COUNTAL.
ZIP: 60610
COMPUTER REALDABLE FORM:
MEDIUM TYPE: Floppy Disk
MEDIUM TYPE: IBM PC Compatible
TWOTTEN: PC-DOS/MS-DOS
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                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,607
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
                                 TELECOMMUNICATION INFORMATION:
                                                  FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No: 5792627thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:051
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5756290thrup
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: Amino acids
STRANDEDNESS: Single
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 APAPASAPAAAAPAGAGTPVTAPLAGTIWKVLASEGQTVAAGEVLLILEAMKMETEIRAA 139
                                                                                                                      APPLICATION NUMBER: 07
FILING DATE: 10/21/92
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                TELEPHONE:
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5. 5792627
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                                                                                                                                                                                                                                                                                                                                                                          Illinois
                                                                                                                                                                                                                                                                                                                                                                                                           321 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robert Haselkorn and Piotr Gornicki
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1-312-755-4489
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                  1-312-744-0090
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5792627th Clark Street
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52.9%;
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                                                                                                                                         07/956,700
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; Pred. No. 6.9e-14;
10; Mismatches 29;
                                                     ARCD: 058
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US-08-475-879-106
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Best Local S
Matches 45
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                                                              Matches
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                                                                                                                                                                                                                                     TELEFAX: 1-312-755-444
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acid
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NAME: Thomas E. No. 5972644 5786170thrup
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII-DOS CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-Coa
TITLE OF INVENTION: Carboxylase
                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 APAPAAGGAGKAGEG-EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96
                            38 APAPAAGGAGAGKAGEG-EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96
                                                                                                                                                           STRANDEDNESS: Sir
TOPOLOGY: Linear
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les 45; Conserv
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 90
                                                                Local Similarity
les 45; Conser
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                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 0'FILING DATE: 10/21/92
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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APAPASAPAAAAPAGAGTPVTAPLAGTIWKVLASEGQTVAAGEVLLILEAMKMETEIRAA 139
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o. 5972644
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Amino acid
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321 No. 5972644 5786170th Clark Street
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                                                                                                                                             Peptide
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                                                                             32.6%;
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                                                                           Score 200.5; DB 2
Pred. No. 6.9e-14;
                                                              Mismatches
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                                                                                           DB 2;
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                                                              Indels
                                                                                           Length 165;
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5252466-19
;Patent No. 5252466
; APPLICANT: CRONAN, JOHN E.
; TITLE OF INVENTION: FUSION PROTEINS HAVING
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                                                                                                                                                                                                                                        SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                   PURIFYING THEM
                                                                                                                                                                                                                                                                                                                                                                                                  VIVO POST-TRANSLATION MODIFICATION AND METHODS
                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/433,043B CURRENT FILING DATE: 1999-10-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HASELKORN, ROBERT APPLICANT: GORNICKI, PIOTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 08/475,879 PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: ARCD:338US
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TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 165
TYPE: PRT
                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 354,266
FILING DATE: 19-MAY-1989
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 QAGTVRGIAVKAGDAVAVGDTLMTL 164
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                                                     97 TDGKVEKVLVKERDAVQGGQGLIKI 121
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/
FILING DATE: 18-MAY-1990
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                                                                                     38 APAPAAGGAGAGKAGEG-EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96
                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                     LENGTH: 100
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45; Conservative
                                                                                                                              Conservative
                                                                                                                                               31.5%; Score 193.5; 51.8%; Pred. No. 2e
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                                                                                                                            Indels
                                                                                                                                                          Length 100;
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SEQ ID NO 2
LENGTH: 1140
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Best Local Similarity
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Best Local S
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SEQ ID NO 2
LENGTH: 1140
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APPLICANT: Lessard, Philip A.
APPLICANT: Willis, Laura B.
APPLICANT: Stephanopoulos, Gregory
TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
FILE REFERENCE: 1533.0790000
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APPLICANT: Lessard, Philip A.
APPLICANT: Willis, Laura B.
APPLICANT: Stephanopoulos, Gregory
TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
FILE REFERENCE: 1533.0790000
CURRENT APPLICATION NUMBER: US/09/220,081
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/220,081 PRIOR FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/677,575
CURRENT FILING DATE: 2000-10-03
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                                                                                                                                                                     25.9%; Score 159.5; DB 4; 43.2%; Pred. No. 1.6e-08;
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43.28;
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Pred. No. 1.6e-08;
5; Mismatches 26;
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RESULT 23
US-08-997-362-166
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US-08-997-080-166
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APPLICATION NUMBER:
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APPLICANT: TAN, PAUL L.J.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
                                                TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MYCOBACTERIAL INFECTIONS
                                                                                                                                                            APPLICANT:
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Scott, Linda
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Visser, Elizabeth
                                                                              Prestidge, Ross
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Pred. No. 8.5e-09;
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US-09-095-855-166
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APPLICANT:
APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: CICALI
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
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                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CLASSIFICATION:
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ARE: FastSEQ for Windows Version APPLICATION DATA:
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Skinner, Margot
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01 Elliott Avenue, Suite 4185
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for Windows Version
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                                                                                                                                                                                                             and Methods for and Diagnosis of Mycobacterial Infections
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US-09-324-542-166
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                                                                                                                                                           Query Match
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LENGTH: 108
                                                                                                                             Matches
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders FILE REPERENCE: 11000 1107c1 CURRENT APPLICATION NUMBER: US/09/324,542 CURRENT FILING DATE: 1999-06-02 EARLIER APPLICATION NUMBER: US 08/997,080 EARLIER FILING DATE: 1997-12-23 NUMBER OF SEO ID NOS: 194
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                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Watson, James D.
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SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                              112 VQGGQGLIKIG 122
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                             33
                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 VDPGTPLVVVG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 GDERVDAPFASSVWKVDVAVGDRVVAGQPLLALEAMKMETVLRAPADGVVTQILVSAGHL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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VDPGTPLVVVG 103
                                                          GDERVDAPFASSVWKVDVAVGDRVVAGQPLLALEAMKMETVLRAPADGVVTQILVSAGHL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65, Application US/09324542
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                                                                                                                           Conservative
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                                                                                                                                          24.48;
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                                                                                                                        Score 150; DB 4;
Pred. No. 8.5e-09;
0; Mismatches 28;
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; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-205-426-166
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TENGTH: 108
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US-09-205-426-166
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Best Local Similarity 46.5%;
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APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment
TITLE OF INVENTION: Diagnosis of Mycobacterial Infection
FILE REFERENCE: 11000.1002c4
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NUMBER OF SEQ ID NOS: 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 09/095,855 EARLIER FILING DATE: 1998-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/205,426 CURRENT FILING DATE: 1998-12-04
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CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
LAW Offices of Ann W. Speckman
ADDRESSEB: Law Offices of Ann W. Speckman
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                      FILING DATE:
                                                                                                                                                                                                    COUNTRY: UZIP: 98121
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                                                                       APPLICATION NUMBER:
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Treatment and
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08/705,347
                                                                       us/09/095,855
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Pred. No. 8.5e-09;
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FILING DATE: 23-DEC-1997 ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: FILING DATE: 12-JUN APPLICATION NUMBER:

12-JUN-1997 UMBER: 08/997,362 23-DEC-1997

29-AUG-1996

08/873,970

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US-09-205-426-199
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EARLIER APPLICATION NUMBER: 05/09/205,426
EARLIER APPLICATION NUMBER: 09/095,855
EARLIER FILING DATE: 1998-06-11
EARLIER FILING DATE: 1997-12-362
EARLIER FILING DATE: 1997-12-37
EARLIER APPLICATION NUMBER: 08/873,970
EARLIER FILING DATE: 1997-06-12
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APPLICANT: Watson, James D
APPLICANT: Tan, Paul L. J.
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                                                                                                                            Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 08/705,347 EARLIER FILING DATE: 1996-08-29
                                                                                                                                                                                                             LENGTH: 243
TYPE: PRT
ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITLE OF INVENTION: Compounds and Methods for Treatment and ITLE OF INVENTION: Diagnosis of Mycobacterial Infections TLE REFERENCE: 11000.1002c4
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REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
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112 VQGGQGLIKIG 122
                                                168 GDERVDAPFASSVWKVDVAVGDRVVAGQPLLALEAMKMETVLRAPADGVVTQILVSAGHL 227
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TELEFAX: 206-269-0563
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linear
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                                                                                                                      24.4%; Score 150; DB 4; Length 243; 46.5%; Pred. No. 2.3e-08; tive 10; Mismatches 28; Indels
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Pred. No. 2.3e-08;
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US-09-134-001C-3428
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Search completed: May 1, 2003, 07:59:04 Job time: 17.6146 secs
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5252466-5
;Patent No. 5252466
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                                                                                                                                                                                                                                                            FILING DATE:
SEQ ID NO:5:
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3428
LENGTH: 1154
                                                                                                                                                 Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/52
FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 354,266
FILING DATE: 19-MAY-1989
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
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APPLICANT: CRONAN, JOHN E.
TITLE OF INVENTION: FUSION PROTEINS HAVING
TITLE OF INVENTION MODIFICATION AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1127 DGIIKQINVANGDAIATGDLLVEI 1150
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                                                                                          58 APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 115
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                                                                                                                                                                                                                                                 LENGTH: 67
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                                                                                                                                                                      Score 137; DB 6; Pred. No. 1.1e-07;
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Pred. No. 2.1e-07;
3; Mismatches 41
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 107, Application US/07956700B Patent No. 5539092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                         COUNTING COUNTING COUNTING COUNTING COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
MEDIUM TYPE: Floppy Disk
TOWNTER: IBM PC Compatible
TOWNTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                        NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/
FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                  SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19921002
                                                                                                                                                       CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
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                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                         DEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
       LENGTH: LL.
                                                                                                              NAME: Thomas E. No. 5539092thrup REGISTRATION NUMBER: 33,268 REFERENCE/DOCKET NUMBER: ARCD:05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
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 STRANDEDNESS:
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                       123 amino acids
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RVENTION: Cyanobacterial and Plant Acetyl-Coa
RVENTION: Carboxylase
                                                                     1-312-755-4489
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1 No. 5539092th Clark Street
                                                                                   1-312-744-0090
Single
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Pred. No. 1.2e-38;
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; MOLECULE TYPE: Peptide
US-07-956-700B-107
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ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
MEDIUM TYPE: IBM PC Compatible
TYPEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                          TELEFAX: 1-312-755-44
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Chicago
CITY: Chicago
TTATE: Illinois
TTSA
                                                                                                                                                                                                                                                                                NAME: Thomas E. No. 5756290thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5756
                                                                                                                                                       TOPOLOGY: L
MOLECULE TYPE:
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 61 QGGQGLIKIG 70
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RVENTION: Cyanobacterial and Plant Acetyl-Coa
RVENTION: Carboxylase
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                                                                                    Conservative
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1 No. 5756290th Clark Street
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                                                                                 Score 342; DB 1;
Pred. No. 1.4e-38;
; Mismatches 0;
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Pred. No. 1.4e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5792627thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
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                                                      APPLICANT: Robert Haselkorn and Piotr Gornicki
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-Coa
TITLE OF INVENTION: Carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 1-312-744-0090
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                              CORRESPONDENCE ADDRESS
                                            NUMBER OF SEQUENCES:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                               54
 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                       QGGQGLIKIG 70
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E: Arnold, White & Durkee 321 No. 5972644 5786170th Clark Street
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VENTION: Cyanobacterial and Plant Acetyl-CoA
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SYSTEM: PC-DOS/MS-DOS
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11 No. 5792627th Clark Street
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Pred. No. 1.4e-38;
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; TYPE: Amino acid
; STRANDEDNESS: Sing
; TOPOLOGY: Linear
; MOLECULE TYPE: Pepti
US-08-475-879-107
                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6072039
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION
                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                            APPLICANT: Haase, Ferdina
APPLICANT: Cress, Dean E
                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                               COUNTRY: UZIP: 19105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Thomas E. No. 5972644 5786170thrup REGISTRATION NUMBER: 33,268
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SOFTWARE: ASCII-DOS
 CLASSIFICATION:
               CLASSIFICATION:
                                CLASSIFICATION:
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                                                             APPLICATION NUMBER: U: FILING DATE: 19910520
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                                                                                                                                                                                                                                             Philadelphia
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ilarity 100.0%;
Conservative
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C07K15/26
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C12P21/00
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Pred. No. 1.4e-38;
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Gaps

TELECOMMUNICATION INFORMATION: TELEPHONE: 215-592-2478

REFERENCE/DOCKET NUMBER: 89

89-020

ATTORNEY/AGENT INFORMATION:
NAME: Driks, Jordan J.
REGISTRATION NUMBER: 22,

435/69.51

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; OTHER INFORMATION: Description ; OTHER INFORMATION: Peptide US-09-433-043B-107
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Query Match
                                                                                                                            SEQ ID NO 107
LENGTH: 123
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Best Local 9
                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/475,879
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                   APPLICANT: HASELKORN, ROBERT
APPLICANT: GONICKI, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ARCD:338US
                                                                                                                                                           SOFTWARE: PatentIn Ver.
                                                                                                                                                                           NUMBER OF SEQ ID NOS: 128
                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 07/956,700 PRIOR FILING DATE: 1992-10-02
                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 215-592-2682
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                            TYPE: PRT
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DATE: NO. 6072039 26-1979
RELEVANT RESIDUES IN SEQ ID NO:
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Bowien, B U
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Zwolinski, G K
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Pred. No. 1.4e-38;
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US-09-364-083-2
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US-09-364-083-2
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SEQ ID NO 2
LENGTH: 194
TYPE: PRT
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Best Local
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PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin V
SEQ ID NO 2
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APPLICANT:
                                                                                                                                                                                                                                                                                  Patent No.
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                                                                                  TITLE OF INVENTION: Compositions and Metl TITLE OF INVENTION: Epitope(s) of Borrell TITLE OF INVENTION: Protein C (OSPC) for TITLE OF INVENTION: Lyme Disease FILE REFERENCE: B. burgdorferi OSPC CURRENT APPLICATION NUMBER: US/09/651,419 CURRENT FILLING DATE: 2000-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOSITIONS and Method Using the Borreliacidal TITLE OF INVENTION: Epitope(s) of Borrelia Burgdorferi Outer Surface TITLE OF INVENTION: Protein C (OSPC) for the Diagnosis and Prevention TITLE OF INVENTION: Lyme Disease FILE REFERENCE: B. burgdorferi OSPC
                                                                   PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                   APPLICANT:
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114 QGGQGLIKIG 12:
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                                                                                                                                                                                                                                                                                  2, Application US/09651419
5. 6464985
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Schell, Ronald F
                                                                                                                                                                                                                                                  Callister,
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                     Ver.
                                                    1998-07-31
                                                                                                                                             Compositions and Method Using the Borreliacidal Epitope(s) of Borrelia Burgdorferi Outer Surface Protein C (OSPC) for the Diagnosis and Prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                2000-08-30
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                                                                   60/094,955
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Pred. No. 2.6e-38;
Nismatches 0;
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; Mismatches 0;
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; TŸPE: PRT
; ORGANISM: Borrelia burgdorferi
US-09-651-419-2
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                                                                                                                                                                                                                                             RESULT 11
5252466-1
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5252466-1
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                                                                                                                                                                             TITLE OF INVENTION: FUSION PROTEINS HAVING VIVO POST-TRANSLATION MODIFICATION AND METHODS
                                                                                                                                                                                                                                Patent No.
                            SEQ ID NO:1:
                                                                                                                                                               PURIFYING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 07/9
PRIOR FILING DATE: 1992-10-02
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HASELKORN, ROBERT APPLICANT: GORNICKI, PIOTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 08/PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                             FILING DATE: 18-MAY-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: 354,
                                                                                                                           NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: GORNICKI, PIOTR
ITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
                                                                                                                                                                                              APPLICANT: CRONAN, JOHN E. TITLE OF INVENTION: FUSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113
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                                                 FILING DATE:
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                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
mes 70; Conserv
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                                                                                                                                                                                                                              5252466
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Pred. No. 9.2e-38;
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                                                                                                                                                                              of A
                                                                                                                                                                                          SITE FOR IN
                                                                                                                                                                             MAKING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 123;
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US-07-687-819-2
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                                                                                                                US-07-687-819-2
                                                       Matches
                                                                    Query Match
Best Local Similarity
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Patent No. 6072039
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Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: AMINO ACID
                                                                                                                           MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435/69.5
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                NAME: Driks, Jordan J
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GLIKIG 66
                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: UPPLING DATE: 19910520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Rohm and Haas Company STREET: Independence Mall West
                5 PAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDG 47
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PAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDG
                                                       43;
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                                                       Conservative
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internal
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C07K15/26
                                                                                                                                                                                                                                                                   NUMBER:
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                                                                  61.7%;
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                                                                  Score 211; DB 3
Pred. No. 1.4e-
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Pred. No. 1.2e-34;
0; Mismatches 2
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
                                                                                DB 3;
                                                                             Length 43;
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43
                                                     Indels
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RESULT 13 US-09-433-043B-127 ; Sequence 127, Application US/09433043B

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RESULT 14
US-07-956-700B-106
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-09-433-043B-127
                                                                                                                                                                                                                                                                                                         COUNTY: 60610
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
MEDIUM TYPE: IBM PC Compatible
TOWNTER: THE PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 106, Application US/07956700B Patent No. 5539092
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LENGTH: 170
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PRIOR TILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/956,700
PRIOR FILING DATE: 1992-10-02
                                                                           TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
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CURRENT FILING DATE: 1999-10-25
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TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ARCD:338US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
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                                                                                                             NAME: Thomas E. No. 5539092thrup REGISTRATION NUMBER: 33,268 REFERENCE/DOCKET NUMBER: ARCD:056 TELECOMMUNICATION INFORMATION: TELEPHONE: 1-312-744-0090
                                                                                                                                                                                                                                                    SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19921002
                                                                                                                                                                                                           CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 DTLMTL 169
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STRANDEDNESS:
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                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chicago
: Illinois
                                  165 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robert Haselkorn and Piotr Gornicki
VENTION: Cyanobacterial and Plant Acetyl-Coa
VENTION: Carboxylase
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5539092th Clark Street
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                                                                                                                                                        ARCD: 058
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Pred. No. 7.5e-15;
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                                                                                                                                                          US-08-476-537-106
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US-08-476-537-106
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Best Local Similarity 53.0
Matches 35; Conservative
                                                                                            Matches
                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 106, Application US/08476537 Patent No. 5756290
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                                                                                                                                                                                                                                                                 TELEPHONE: 1-312-744-0090
TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 100
                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5756290thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:056
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
FILING DATE: 10/21/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                       TOPOLOGY: L
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5756290th Clark Street
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Lbm ... PC
OPERATING SYSTEM: PC
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64 QGLIKI 69
                               99
                                                                                                                                                                                                   STRANDEDNESS:
                                                 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 OGLIKI 69
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                               VTAPLAGTIWKVLASEGQTVAAGEVLLILEAMKMETEIRAAQAGTVRGIAVKAGDAVAVG 156
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                                                                                                                                                                                                                     Amino acid
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NVENTION: Cyanobacterial and Plant Acetyl-Coa
NVENTION: Carboxylase
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                                                                                            Conservative
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                         Linear
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                                                                                          Score 165; DB 1;
Pred. No. 1.3e-14;
9; Mismatches 22
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Pred. No. 1.3e-14;
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                                                                                                                      Length 165,
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Best Local Similarity
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                                                                                                                                                                                                Sequence 106, Application US/08475879
                                                                                                                                                              Patent No. 5972644
Patent No. 5972644 5786170
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                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                NUMBER OF SEQUENCES:
                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
RATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5792627thrup
REGISTRATION NUMBER: 33,268
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                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                               159 DTLMTL 164
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   STATE:
                                   STREET:
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Chicago
: Illinois
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Amino acid
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                                5: Arnold, White & Durkee
321 No. 5972644 5786170th Clark Street
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321 No. 5792627th Clark Street
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                                                                                                                                Robert Haselkorn and Piotr Gornicki
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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ENTION: Cyanobacterial and Plant Acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                Cyanobacterial and Carboxylase
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Pred. No. 1.3e-14;
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                                                                                                                 Plant Acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 165;
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Query Match
Best Local Similarity
Thes 35; Conserve
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                                                                                    ; OTHER INFORMATION: ; OTHER INFORMATION: US-09-433-043B-106
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                                                                                                                                                                                      SOFTWARE: PatentIn Ver.
SEQ ID NO 106
LENGTH: 165
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Best Local Similarity
Matches 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 106, Application US/09433043B Patent No. 6399342
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HASELKORN, ROBERT
APPLICANT: GORNICKI, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/475,879 PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/433,043B CURRENT FILING DATE: 1999-10-25
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 128
                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 07/956,700
                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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TOPOLOGY: Lin
MOLECULE TYPE:
                                                                                                                                        FEATURE:
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APPLICATION NUMBER: 07/9:
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Thomas E. No. 5972644 5786170thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
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                                                                                                                                                                                                                                                            1992-10-02
                                                                                                    Description of Artificial Sequence: Peptide
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                                  48.2%;
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                                Score 165; DB 4; Length 165; Pred. No. 1.3e-14;
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Pred. No. 1.3e-14;
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5252466-19
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                                                                                                                                                                             SEQ ID NO 2
LENGTH: 1140
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
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Best Local Similarity
Matches 34; Conserv
                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Applic Patent No. 6171833
                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/220,081
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                              SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                APPLICANT: Willis, Laura B.
APPLICANT: Stephanopoulos, Gregory
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sinskey, Anthony J. APPLICANT: Lessard, Philip A.
                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
 1131
                           » 61
                                                      1072 KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVPAATKV 1130
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CRONAN, JOHN E.
                                                                                                           Local 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 DTLMTL 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/525,568 FILING DATE: 18-MAY-1990
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EGGDLIVVV 1139
                         QGGQGLIKI 69
                                                                     EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
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                                                                                                                             Similarity
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51.5%;
                                                                                                            45.5%; Score 155.5; DB 4;
44.9%; Pred. No. 3.4e-12;
tive 14; Mismatches 23;
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Pred. No. 6e-14;
9; Mismatches 23;
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OF MAKING !
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US-09-677-575-2
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APPLICANT: Sinskey, Anthony J.
APPLICANT: Lessard, Philip A.
APPLICANT: Willis, Laura B.
APPLICANT: Willis, Laura B.
APPLICANT: Stephanopoulos, Gregory
TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
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LENGTH: 1140
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Patent No. 6403351
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PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 36
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                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                        ATTORNEY/AGENT INFORMATION: NAME: Sleath, Janet
                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE
TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WATSON, JAMES D. APPLICANT: TAN, PAUL L.J.
                                   NAME: Sleath, Janet REGISTRATION NUMBER: 37,007 REFERENCE/DOCKET NUMBER: 11
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                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                        APPLICATION NUMBER:
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o. 5968524
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01 Elliott Avenue, Suite 4185
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Pred. No. 3.4e-12;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

166:

ENGTH:

STRANDEDNESS:

amino acid

108 amino acids

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RESULT 23
US-08-997-362-166
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Best Local Similarity
 Query Match
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                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                            FILING DATE: August 29, ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                NAME: Sleath, Janet REGISTRATION NUMBER: 37,007 REFERENCE/DOCKET NUMBER: 11
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                                                         STRANDEDNESS:
                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                        APPLICATION NUMBER: U.S. Patent Application No. FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. FILING DATE: August 29, 1996
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                     ICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                 ARE: FastSEQ for Windows Version 2.0 APPLICATION DATA:
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                                                                         amino acid
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2601 Elliott Avenue, Suite 4185
                                                                                      108 amino acids
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Scott, Linda
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Pred. No. 5e-12;
 Score 144;
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64 QGLIKIG 70 |: :|

37 VDAPFASSVWKVDVAVGDRVVAGQPLLALEAMKMETVLRAPADGVVTQILVSAGHLVDPG 96

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US-09-095-855-166
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                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                                        Local Similarity
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TOPOLOGY: linear
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                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                               FILING DATE: 12-JU
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/7 FILING DATE: 29-AUG-1996
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4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
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5. 6160093
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                                                                                                                                                 amino acid
                                                                                                                                                              108 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                              UMBER: 08/997,362
23-DEC-1997
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47.88;
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                                                                                                                                                                                                                                                                         11000.1002c3
                                       Score 144; DB 4
Pred. No. 5e-12;
9; Mismatches
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                                                                       DB 4; Length 108
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                                                                                                                                   ; ORGANISM: Mycobacterium vaccae US-09-205-426-166
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US-09-205-426-166
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US-09-324-542-166
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                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 09/095,855
EARLIER FILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER FILING DATE: 1997-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment
TITLE OF INVENTION: Diagnosis of Mycobacterial Infection
FILE REFERENCE: 11000.1002c4
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Methods and Compounds for the TraTITLE OF INVENTION: of Immunologically-Mediated Skin FILE REFERENCE: 11000.1007c1
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                              EARLIER FILING DATE: 1996-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: US 08/997,080 EARLIER FILING DATE: 1997-12-23
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                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE:
                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 08/873,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                        ENGTH: 108
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                                                                            Local Similarity
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4. IPAPLAGTVSKILVKEGDTVKAGOTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
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                                                         9;
                                                                        Score 144; DB 4;
Pred. No. 5e-12;
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Pred. No. 5e-12;
                                                          Mismatches
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APPLICATION NUMBER: 0
FILING DATE: 29-AUG-1
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Compounds and Methods for TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
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                                                             172 VDAPFASSVWKVDVAVGDRVVAGQPLLALEAMKMETVLRAPADGVVTQILVSAGHLVDPG 231
232 TPLVVVG 238
                            64 QGLIKIG 70
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                                                                                                                        Local Similarity es 32; Conserv
                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                        4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
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                                                                                                                   Pred. No. 1.5e
9; Mismatches
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Pred. No. 1
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1.5e-11;
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RESULT

Patent No.

640670

Application US/09205426

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US-09-134-001C-3428
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; LENGTH: 1154
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3428
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; TYPE: PRT
; ORGANIZM: Mycobacterium vaccae
US-09-205-426-199
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 199
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APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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CURRENT FILING DATE: 1998-08-13
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CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 09/095,855
EARLIER FILING DATE: 1998-06-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPLICANT: Lynn Doucette-Stamm et al IIIILE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILLE REFERENCE: GTC-007
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EARLIER FILING DATE: 1996-08-29
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EARLIER FILING DATE: 1997-12-23
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1145 DLLVEI 1150
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                                                                          1085 IGAQMPGSVTEVKVSVGDEVQANQPLLITEAMKMETTIQAPFDGIIKQINVANGDAIATG 1144
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                                       64 QGLIKI 69
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                                                                                                                                                                             Local Similarity
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                                                                                                    4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63.
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FILING DATE: 1997-06-12
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;Patent No.
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LENGTH: 67
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TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
PURIFYING THEM
                                                                                                                                                     Query Match 40.1
Best Local Similarity 50.0
Matches 29; Conservative
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 354,266 FILING DATE: 19-MAY-1989
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                                                                                                                 6 APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG
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biotin carboxylase

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acetyl-CoA carboxy hypothetical prote hypothetical pyruvate carboxyla

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Result No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-123 <MAL>
C; Comment: Six or 12 chains of biotin carboxyl carrier protein (BCCP) are found conzyme A to BCCP and (2) from BCCP to pyruvate, forming oxalacetate.
C; Comment: See PIR:A48665 and PIR:S36808.
C; Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology C; Keywords: biotin binding
C; Keywords: biotin binding
C; Keywords: biotin binding
C; Keywords: biotin binding homology <LPB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  blotin carboxyl carrier protein [validated] - Propionibacterium freudenreichii subsp. sh R;Alternate names: methylmalonyl-CoA carboxyltransferase biotin carboxyl carrier protein C;Species: Propionibacterium freudenreichii subsp. shermanii C;Date: 31-Mar-1980 #sequence_revision 31-Mar-1980 #text_change 01-Feb-2002 C;Accession: A03401
                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-145 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999
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A;Title: Amino acid sequence of the biotinyl subunit from A;Reference number: A03401; MUID:80049796; PMID:40985
A;Accession: A03401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PA---AGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPT 97
                                                                             MKVKVVVNGKEYEVDVEEVMPGKFRVTLEGKTYEVEANLGIQVAPVQTQVATPAPTPTPT
                                                                                                                     MKLKVTVNGTAYDVDVD------VDKSHE-----NPMGTILFGGGTGGAPA 40
PTPVQAPTTPQVQASENVVTAPMPGKVLKILVQEGQQVKLGQGLLILEAMKMENEIPAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI
                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F75135
                                                                                                                                                                                                                                           biotin carboxyl carrier protein; lipoyl/biotin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bowien, B.U.; Zwolinski, G.K.; Kumar, K.G.; Wood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                  37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  abyssi genome sequence:
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                                                                                                                                                                                  Score 231.5;
Pred. No. 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 604.5;
Pred. No. 2.
                                                                                                                                                               Mismatches
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                                                                                                                                                                                      .2e-11
                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              insights into archaeal chromosome str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrococcus abyssi (strain
                                                                                                                                                               Indels
                                                                                                                                                                                                   Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcarboxylase
                                                                                                                                                               23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H.G.; Ericsson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                           homology
                                                                               60
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                                                                                                                                                                                                                                                                                                                                                                                                                     methylmalonyl-COA decarboxylase (EC 4.1.1.41) gamma chain - Veillonella par
C;Species: Veillonella parvula
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C;Accession: D49094
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D49094
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C:Superfamily: biotin carboxyl carrier
F:76-149/Domain: lipoyl/biotin-binding
                   RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AP000005; NID:g3236132; PIDN:BAA30387.1; PID:g3257704
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: A71074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable methylmalonyl-CoA decarboxylase gamma chain - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession:
R; Kawarabayas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-149 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics
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                                                                             124 RDGVVKRILVKEGEAVDTGQPLIELG
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                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                1 MKLKVTVNGTAYDVDVD--------VDKSHENPMGTILFGGGTG
                                                                                                                      TDGKVEKVLVKERDAVQGGQGLIKIG
                                                                                                                                                        PTPTPAPAPSSKTVVSENVVSAPMPGKVLRVLVRVGDRVRVGQGLLVLEAMKMENEIPSP 123
                                                                                                                                                                                                                                        MKVKVVVNGKEYEVEVEEVMPGKFRVTLEGETYEVETSAGFVTSPKQVQVPTPAPTPAPA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGKVEKVLVKERDAVQGGQGLIKIG
                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y.; Sawada, M.;
Funahashi, T.;
                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                             35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an interim accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horikawa, H.; Haikawa,
Tanaka, T.; Kudoh, Y.;
                                                                                                                                                                                                                                                                                                                                             Score 221; DB 2; Pred. No. 8.6e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                         protein; lipoyl/biotin-binding
homology <LPB>
                                                                                                                                                                                                                                                                                                                                                                Length 149
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; Yamazaki,
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome of a hyper-thermophili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence replaced
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J.; Kushida,
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A;Cross-references: GB:L22208; NID:g415592; PIDN:AAC36823.1; PID:g415596 C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding hom C;Keywords: carbon-carbon lyase; carboxy-lyase P;57-129/Domain: lipoyl/biotin-binding homology <LPB> R;Huder, J.B.; Dimroth, P.
J. Blol. Chem. 268, 24564-24571, 1993
A;Title: Sequence of the sodium ion pump methylmalonyl-CoA A;Reference number: A49094; MUID:94043308; PMID:8227015
A;Accession: D49094
A;Status: preliminary A; Molecule type: DNA A; Residues: 1-129 <HUD> Query Match Best Local ω KLKVTVNGTAYDVDVDVS---HENPMGTILFGGGTGGAPAPAAGGAGAG---KAGEGE 55 KENVTVNGTAYDVEVNEVKAAAPAAAPKAAPAAAPAAAPAPAPAPAPAAAAAPVPAGAET 62 Similarity 33.3%; Score 205; DB 2; Pred. No. 1.4e-09; Length 129; Indels decarboxylase from Veillon Gaps 2

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A; Note:
C; Superf
C; Keywor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oxaloacetate decarboxylase (EC 4.1.1.3) alpha chain - N;Alternate names: oxalate beta-decarboxylase, alpha cC;Species: Klebsiella pneumoniae
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                                                                                                                                                                                           C; Complex: heterotetramer [validated, MUID: 98088990]
                                                                                                                                                                                                                                                    A; Experimental source: DSM 2376
C; Comment: Methylmalonyl-CoA decarboxylase catalyses the clock is coupled to the vectorial transport of Na+ across
                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-134 <BOT>
                                                                                                                                                                                                                                                                                                                                                                                                         R:Bott, M.; Pfister, K.; Burda, P.; Kalbermatter, O.; Woehlke, G.; Dimroth, P. Eur. J. Biochem. 250, 590.599, 1997
Bur. J. Biochem. 250, 590.599, 1997
A;Title: Methylmalonyl-CoA decarboxylase from Propionigenium modestum: Cloning A;Reference number: Z22888; MUID:98088990; PMID:9428714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Date: 21-Ja
C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methylmalonyl-CoA decarboxylase (EC 4.1.1.41) gamma chain [imported] - Propionigenium C; Species: Propionigenium modestum
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A;Title: The sodium ion translocating oxalacetate decarboxylase of Klebsiella
A;Reference number: A28088; MUID:88257085; PMID:2454915
A;Accession: A28088
                                                                                                                                                         A; Description:
                                                                                                                                                                             C; Function:
                                                                                                                                                                                                               A; Note: mmdC
                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AJ002015; NID:g2706397; PIDN:CAA05139.1; PID:g2706400
                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: T44984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 11-Jan-2002;Accession: A28088
                                                                                                                 Note: specific activity up to 25 U/mg protein; Superfamily: biotin carboxyl carrier protein;
                                                                                                                                                                                                                                    Genetics:
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Best Local
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                      . Similarity
52; Conser
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                                                                                                                                                         EC 4.1.1.41 [validated, MUID:98088990]
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                      Conservative
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                                    32.3%;
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                                                                                            Lyase;
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                    : Score 198.5;
Pred. No. 4.7e
12; Mismatches
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Pred. No. 1.5e
10; Mismatches
                                                                                              carboxy-lyase
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                                        4.7e-09;
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                                                                                                                 ; Km value for (S)-methylmalonyl-CoA lipoyl/biotin-binding homology
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                                                            134;
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cytoplasmic membrane,
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                          A; Residues: 1-140 <KLE>
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C;Date: 08-May-1998 #sequence_revision
C;Accession: B70432
                                                                                        A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: H69526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
B70432
  A;Cross-references: G
C;Superfamily: biotin
                                                                                                                                                                                     .; Fleischmann, R.D.; Quackenbush, Glodek, A.; Zhou, L.; Overbeek, R. Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                    methylmalonyl-CoA decarboxylase, biotin carboxyl carrier subunit (mmdC) home C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Aug-1999 C;Accession: H69526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The complete genome of the A;Reference number: A70300; MUID:981 A;Accession: B70432 A;Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pyruvate carboxylase c-terminal
C; Species: Aquifex aeolicus
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                                                                                                                                                                                                                              R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; K
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                                                                      A; Status: preliminary; nucleic
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Best Local Similarity
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GB:AE000952;
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carrier protein;
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                                                                                                                                                                                                             R.;
                                                                        sequence
                                                                                                                                                                                                             Gocayne, J.D.;
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not

shown;

translation

not

Weidman,

J.F.; McDonald,

Kirkness, K.A.,

s, E

homolog

Arc

P.; Kaine,

B.P.;

Sykes,

NID:g2689275; PIDN:AAB89036.1; n; lipoyl/biotin-binding homolo

PID:g264

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115
                                                                                                                                                                                                                                C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase F;572-646/Domain: lipoyl/biotin-binding homology <LPB> F;612/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                           KFKVRIEGVSVDAESGKPRKYYVRINNRLEEIQLKPFKEAIPQGGGAQTVQSAEEEEGIP
                                    KAGE-GEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKE 108
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KATEPGDVTPPMPGKVVKILVKEGEPVQQGQTVATVEAMKMENEVHAPIDGIVKKIFAKP
                                                                                                                                                                                                                                                                                                                                                      GB:AE000744; NID:g2983891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    e of the hyperthermophilic bacterium MUID:98196666; PMID:9537320
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                                                                                                                  -VDVDKSHE----NPMGTILFGGGTGGAPAPAAGGAGAG
                                                                                                                                                    Score 190.5; DB 2;
Pred. No. 9.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                             sequence not shown;
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    Aquifex aeolicus

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G82308

Oxaloacetate decarboxylase, alpha chain VC0550 [similarity]

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: G82308

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.;

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I
           A;Title: DNA Sequence of both chromosomes of the cholera A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: G82308 A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA
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G82308
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: D81367
A; Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Parkhill, J.; Wren, B.W.; Mungall, K.;
C.W.; Quail, M.; Rajandream, M.A.; Ruther
Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable pyruvate carboxylase (EC 6.4.1.1) B chain C;Species: Campylobacter intent
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A; Residues: 1-599 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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35.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 187.5; DB 2;
Pred. No. 1.6e-07;
5; Mismatches 40;
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pred. No. 2.3e-08;
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                                                                                                                                                                                                                      VC0550 [similarity] - Vibrio cholerae
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rford, K.M.; VanVliet, A
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                                                                                  pathogen
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A.; Whitehead,
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                                                                              Vibrio cholerae.
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    Campylobacter

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A; Molecule type: DNA A; Residues: 1-576 < KUR> A; Cross-references: GB:

GB:AE007870;

PIDN: AAK89506.1;

PID:g15159380;

GSPDB:GN00170

A;Status:

preliminary

A; Reference number: A; Accession: H98247 A; Title: Genome Sequence Science 294, 2323-2328, 2001

R; Goodner, B.; Hinkle, G. A.; Liu, F.; Wollam, C.;

G.; Gattung, S.; C.; Allinger, M.;

Miller, N Doughty,

Blanchard, M.; Qurollo, Scott, C.; Lappas, C.;

Lappas,

B.; Gold

GOLdm

C58,

Cer

the Plant Pathogen PMID:11743194

and N. .

Biotechnology

Agent Agrobacterium

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A;Gene: PH0834
C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase
F;498-571/Domain: lipoyl/biotin-binding homology <LPB>
H98247

blotin carboxylase protein A2 [imported] - Agrobacterium tumefaciens (strain c); Species: Agrobacterium tumefaciens (; Species: Agrobacterium tumefaciens C; Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 C; Accession: H98247
                                                                                                                                                                                                                                                                                                                                                                       F;537/Binding site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AP000003; NID:g3236130; A;Experimental source: strain OT3
A;Note: this accession replaces an interim acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Kawarabayasi, Y.; Sawada, M.; Ohfuku, Y.; Funahashi, DNA Res. 5, 55-76, 1998
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C; Accession:
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C; Species: Pyrococcus horikoshii
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C; Superfamily: Klebsiella
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                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-571 <KAW>
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                   Score 184; DB 2; Pred. No. 2.8e-07;
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Yamazaki,
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RESULT
AC3038
biotin
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A; Gene: AGR_L_1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: Atu3913
A;Map position: linear chromosome
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase
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                                                              A; Reference number: A72200; A; Accession: C72341
                                                                                                                                                                         proplonyl-CoA carboxylase, gamma subunit - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C;Accession: C72341
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 A;Cross-references: GB:AE001743;
                A; Residues:
                                  A; Molecule
                                               A; Status: preliminary
                                                                                             Nature 399, 323-329, 1999
A;Title: Evidence for late
                                                                                                                                                        R; Nelson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE008689; PIDN:AAL44721.1; PID:g17742353; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-576 < KUR>
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A;Accession: AC3038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Karp,
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Best Local
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294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                   MGTILFGGGTGGAPAPAAGGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLE 85
                                                                                                                                                       K.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMKMETQIVATRAGKV-RLIVKEGDYLQAGATLIDI 574
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                  type: DNA: 1-134 <ARN>
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42; Conserv
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                                                                                                                                             Stewart,
                                                                                                                                                        Clayton,
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                                                                              lateral gene transfer between Archaea 72200; MUID:99287316; PMID:10360571
                                                                                                                                          , R.A.;
A.M.; C
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43.8%;

    Agrobacterium tumefaciens

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                                                                                                                                           Gill, S.R.;
Cotton, M.D.
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GB:AE000512; NID:g4981241;
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Pred. No. 1.1
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                                                                                                                                           .D.;
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                                                                                                                                          Gwinn, M.L.; Dodson, R.i
; Pratt, M.S.; Phillips,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Engineer
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PIDN: AAD35799.1;
                                                                                             and Bacteria
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                                                                                                                                        R.J.; Hat
lps, C.A.;
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                                         R;Woehlke, G.; Wifling, K.; Dimroth, P.
J. Biol. Chem. 267, 22798-22803, 1992
A;Title: Sequence of the sodium ion pump oxaloacetate decarboxylase from Salmonella A;Reference number: A44465; MUID:93054591; PMID:1331067
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                             A; Reference number: A44465; A; Accession: B44465
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 A; Status: |
A; Molecule
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A; Experimental source: strain c; Genetics:
A; Gene: TM0717
C; Superfamily: biotin carboxyl
sodium ion pump oxaloacetate decarboxylase subunit alpha C;Species: Salmonella typhimurium C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_C;Accession: B44465
                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: pyruvate carboxylase; biotin carboxylase homology;
C;Keywords: ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Date: 21-Jan-2000
C; Accession: T44608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pyruvate carboxylase (EC 6.4.1.1) [imported] - C;Species: Bacilius rereno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-984 < OKS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Genome organisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microbiology 145,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Okstad, O.A.;
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                     970 GDAIQTGDLLIEL
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                                                                                                                                                                                                                             910 NRENPNHISATMPGTVIKVVVKEGDEVKKGDSMAITEAMKMETTVQAPFNGKVKKVYVND
                                                                                                                                                                                                                                                                                                   850 GEEIDVEIEQGKTLMVKLVSIGEPQPDGNRVLYLEFNGQPREIVVKDESVKATVAQRVKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hegna, I.; Lindbaeck, 5, 621-631, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL:AJ010111; NID:g4584147; PIDN:CAB40604.1; pe: ATCC 10987
                                                                                                                                                                                        121
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33.8%;
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Pred. No. 2.8e-07;
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                     #text_change
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                                                        Salmonella typhimurium
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preliminary e type: DNA

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RESULT
D90418
                                                                 hypothetical protein SSO2464 [imported] -
C;Species: Sulfolobus solitatarious
C;Date: 24-May-2001 #sequence_revision 24-
C;Accession: D90418
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G84306
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M. Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
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A; Authors: Hou, S.; Danie
A; Title: Genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: G84306
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.;
A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Halobacterium sp. NRC-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-591 <WOE>
A;Cross-references: GB:M96434; NID:g154195; PIDN:AAA02973.1; PID:g408892
A;Experimental source: LT2
A;Note: sequence extracted from NCBT backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE004437;
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A; Residues: 1-610 <S
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Best Local
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Pred. No. 1.
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                                                                                   24-May-2001 #text_change 24-May-2001
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                                                                                                                            Sulfolobus solfataricus
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  oxaloacetate decarboxylase (EC 4.1.1.3) alpha chain [imported] C;Specites: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AE0909
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard
                                                                                                                               AE0909
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Thomson,

Pickard,

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Wain,

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Church

#text_change

27-Nov-2001

Salmonella

enterica

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oxaloacetate decarboxylase (EC 4.1.1.3) alpha chain [imported] . (;Speciles: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AB0509
                                                                                                                                                                                                         A;Gene: oadA
C;Superfamily: Klebsiella
C;Keywords: carbon-carbon
                                                                                                                                                                                                                                                                                                                                                              Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; A; Title: Complete genome sequence of a multiple A; Reference number: AB0502; PMID:11677608
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C;Genetics:
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A; Residues: 1-591 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Parkhill, J.; Dougan, th, T.; Connerton, P.;
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A; Accession: D90418
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to GenBank, April 2001 A; Description: Sulfolobus solfat
                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                   A; Accession: AB0509
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A; Residues: 1-186 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
                                                                                                                                                            Query Match
Best Local
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                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Connerton,
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WKVIATEGQSVAEGDVLLILEAMKMETEIRAAQAGTVRGIAVKSGDAVSVGDTLMTL
                     SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
                                                                   VEVEGKAFVVRVS-DGGDISQLTTAV--PAASSAPVQAAAPAGAGT----PVTAPLAGNI 533
                                                                                                     VTVNGTAYDVDVDKSHENPMGTILFGGGTGGAPAPAAGGAGAGKAGEGEIPAPLAGTV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQ 116
                                                                                                                                        1 Similarity 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      S.; O'Gaora, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 40.
                                                                                                                                                                                                                           Klebsiella pneumoniae oxaloacetate
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                            GB:AL513382; PIDN:CAD01210.1; PID:g16501339; GSPDB:GN00176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cronin, A.; Davis,
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                                                                                                                                                          40.28;
                                                                                                                                                                          28.28;
                                                                                                                                                                                                           lyase; carboxy-lyase
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                                                                                                                                                        Score 173.5;
Pred. No. 2e-
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Pred. No. 6.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   K.D.; Thomson, N.R.; Pickard,
Davis, P.; Davies, R.M.; Dowd,
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                                                                                                                                        49;
                                                                                                                                                                                                                             decarboxylase
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, L.; White,
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                                                                                                                                    Gaps
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                                                                                                                                                                                                                           chain; lipoyl/b
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te, N.; Farr
                                                                                                                                                                                                                                                                                                                                                                                   enterica
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pyruvate carboxylase, PYKA [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30
C;Accession: D97227
                                                                                      RESULT
D97227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M. A;Title: Complete genome sequence of the methanogenic archaeon, A;Reference number: A64300; MUID:96337999; PMID:8688087
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F64453
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C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Authors: Parry, C.; Quail, M.; Rutherford, K.; A; Title: Complete genome sequence of a multiple dA; Reference number: AB0502; PMID:11677608
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                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase C;Keywords: carbon-carbon lyase; carboxy-lyase C;Keywords: carbon-carbon lyase; carboxy-lyase F;494-567/Domain: lipoyl/biotin-binding homology <LPB>F;533/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Bult, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oxaloacetate decarboxylase (EC 4.1.1.3) alpha chain MJ1231 [similarity] - Methanococcus
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A; Residues: 1-591 <PAR>
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A; Residues: 1-567 <BUL>
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A;Accession: F64453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: F64453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Methanococcus jannaschii;Date: 13-Sep-1996 #text_change 18-Aug-2000;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics
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c.: O'Gaora,
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C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,
; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
                                                                                                                                                                                NVGDVIMII 566
                                                                                                                                                                                                                                                                                                         EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 112
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47; Conserv
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50.7%;
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                                                                                                                                                                                                                                                                                                                                               Score 173; DB 2; Le
: Pred. No. 2.1e-06;
----ches 22;
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                      #text_change 30-Sep-2001
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odek, A.
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oxaloacetate decarboxylase alpha chain -
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08
C;Accession: F70439
                                                                                   RESULT
F70439
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VAKGDRVNPGEILIEI

605

08-May-1998 #text_change Aquifex aeolicus

18-Aug-2000

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A; Gene: PA5435
C; Superfamily:
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A; Gene: CAC2660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
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                                                                                                                                                                                                                                                           A;Cross-references: GB:AE004956; GB:AE004091; A;Experimental source: strain PAO1 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-1144 <KUR>
A; Cross-references: GB:AE001437; PIDN:AAK80607.1; PID:g15025689; A; Experimental source: Clostridium acetobutylicum ATCC824
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                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable transcarboxylase subunit PA5435 [imported] - C;Species: Pseudomonas Aprintinos
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A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                             A; Residues: 1-607 <STO>
                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Complete genome
                                                                                                                                                                                                                                                                                                                                                                                                              .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                              A; Molecule type:
                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession:
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106 VKERDAVQGGQGLIKI
                                                                                             480 IDVHGETYRVDITGVGVKSDNKRHFYLSIDGMPEEVVFEPLNEYVAGSASGRKHA-----
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                                ----SEPGHVSTIMPGNIVDVLVKEGDSVKAGQAVLITEAMKMETEVQAGIAGTVKAIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERDAVQGGQGLIKI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADSSNKKEIGASIPGNVVKVFVKPGDKVKKGDSLMVIEAMKMETNVSVSEDGTVGGIFVK 1129
                                                             AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVL
                                                                                                                             VTVNGTAYDVDV---
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35; Conserv
                                                                                                                                                                               Similarity
                                                                                                                                                                                                                         Klebsiella pneumoniae oxaloacetate decarboxylase alpha
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                                                                                                                                                                                                                                                                                                                               DNA
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                                                                                                                                                                           27.48;
 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 170; DB 2; Pred. No. 7.3e-06;
                                                                                                                                                          Score 168.5; DB 2
Pred. No. 5.1e-06;
0; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                          Coulter, S.N.; Fo
                                                                                                                            ----DVDKSHE----NPMGTILFGGGTGGAPAPAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Smith, D.R.
                                                                                                                                                                                                                                                                                            NID:g9951760;
                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                            PIDN: AAG08820.1;
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Larbig,
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Rajandream, M.A.; Rogers, J.; Nucur., Rajandream, M.A.; Rogers, J.; Nucur., Rajandream, M.A.; Rogers, 1998
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
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A;Atthors: Sqares, R.; Sulston, J.E.; Taylor, R.; Whitehead, S.; Barrell, B.G.
A;Atthors: Sqares, R.; Sulston, J.E.; Taylor, R.; Whitehead, S.; Whitehead, S.; Barrell, R.; Whitehead, S.; Barrell, R.; Whitehead, S.; Barrell, R.; Whitehead, S.; Whitehead, S.; Barrell, R.; Whitehead, S.; Whitehead,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: F70439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: F70980
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A; Residues: 1-620 <AQF>
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; 527-600/Domain: lipoyl/biotin-binding homology <LPB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:Z92771; GB:AL123456; NID:g3242259; PIDN:CAB07068.1; PID:g1877340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene: accA3
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Best Local :
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594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 VTVNGTAYDVDVDVSHENPMGTILFGGGTGG----
TVLAEI 599
                                                         QGLIKI 121
                                                                                                                                                                         IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG
                                                                                                                                                                                                                                         KVVVEIDGRRVEVSLPADLALSNGGGCDPVGVI-----RRKPKPRKRGAHTGAAASGDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGK----AGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVE
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                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                            27.0%; Score 166; DB 2; 1
35.7%; Pred. No. 7.9e-06;
36.7%; Mismatches 51;
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Pred. No. 5.2e-06;
Pred. Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 600
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A;Reference number: A87249; MA;Accession: G87517
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-654 <570>
A;Cross-references: GB:AE0056
C;Genetics:
A;Cene: CC2168
                                                                                                                                                                                                                                                                                                                                                      A; Gene: CC2168
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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G87517
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A; Molecule type: DNA
A; Residues: 1-1150 <STO>
A; Cross-references: GB: AP001516; GB: BA0000004; NID: g10175192;
A; Cross-rental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: G87517
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Takami, H.; Nakasone, K.; Takaki, Y.;
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pyruvate carboxylase pycA [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: A83978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acetyl/propionyl-CoA carboxylase, alpha subunit [imported] -
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Matches 35
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Best Local
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                                                                                      GKGPIQVFEGGDVQEFDFVAKIGGAGEGGASDGAILSPMPGKIVSVSVSAGQTVSKGQTL 609
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                                       LVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQ 116
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35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              GB:AE005673; NID:g13423663;
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                                                                                                                                                                                                                                                                    26.7%; Score 164; DB 2; 31.0%; Pred. No. 1.2e-05; tive 12; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.8%;
                                                                                                                                                                            -----TPLRVALIGGGTEDWSWDIRHADGSTFDEVTRLPTTY 549
                                                                                                                                -APAAGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTV 81
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Pred. No. 1.8e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN: AAK24139.1;
                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                              Length 654
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                                                                                                                                                                                                                                                                       56;
                                                                                                                                                                                                                                                                                                                                                                                                                              GSPDB: GN00148
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C;Accession: G86999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein bccA [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
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                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AL450380; NID:g13092853; PIDN:CAC30235.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-598 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
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A;Accession: G86999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Cole, S.T.;
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    carboxyl carrier protein
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                                                                                                                                                      64 VSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
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                                                                                                                                                                                                  VEVDGRRLEVSLPADLALANPAGCNP-AGVIRKKPKPKRGGHTGAATSGDAVTAPMQGT 539
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                                                                                                           VVKVAVAEGQTVMTGDLVVVLEAMKMENPVTAHKDGIITGLAVEAGTAITQGTVLAEI 597
                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.M.; Devlin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1007-1011, 2001
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                                                                                                                                                                                                                                                                                           Conservative
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37.3%;
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                                                                                                                                                                                                                                                                                                           Score 163; DB 2;
Pred. No. 1.4e-05;
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Pred. No. 3.2e-06;
3; Mismatches 19;
  Mycobacterium
    leprae
                                                                                                                                                                                                                                                                                      57; Indels
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Holroyd,
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C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; li C;Keywords: biotin binding F;I1-463/Domain: biotin carboxylase homology <BCH>F;513-598/Domain: lipoyl/biotin binding homology <LPB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mycobacterium leprae
C;Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 11-Jan-2002
C;Accession: A55579; S22188
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A; Residues: 1-598 < NOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: A55579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Lipid synthesis
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J. Bacteriol. 176, 2525-2531, 1994
                                                                                                                                                                                                      Matches
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540 VVKVAVAEGQTVMTGDLVVVLEAMKMENPVTAHKDGIITGLAVEAGTAITQGTVLAEI
                                                                                               481 VEVDGRRLEVSLPADLALANPAGCNP-AGVIRKKPKPRKRGGHTGAATSGDAVTAPMQGT 539
                                               64 VSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
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                                                                                                                                                                                                   Conservative
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37.3%;
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Pred. No. 1.4e-05;
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Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69510

not shown;

translation not shown

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dc.; Fleischmann, R.D.; Quackenbush, J.; Lee; N.H.; Sutton, G.G.; Glll, S.; Kirkness, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

K.A.; Dodsor irkness, E.F.

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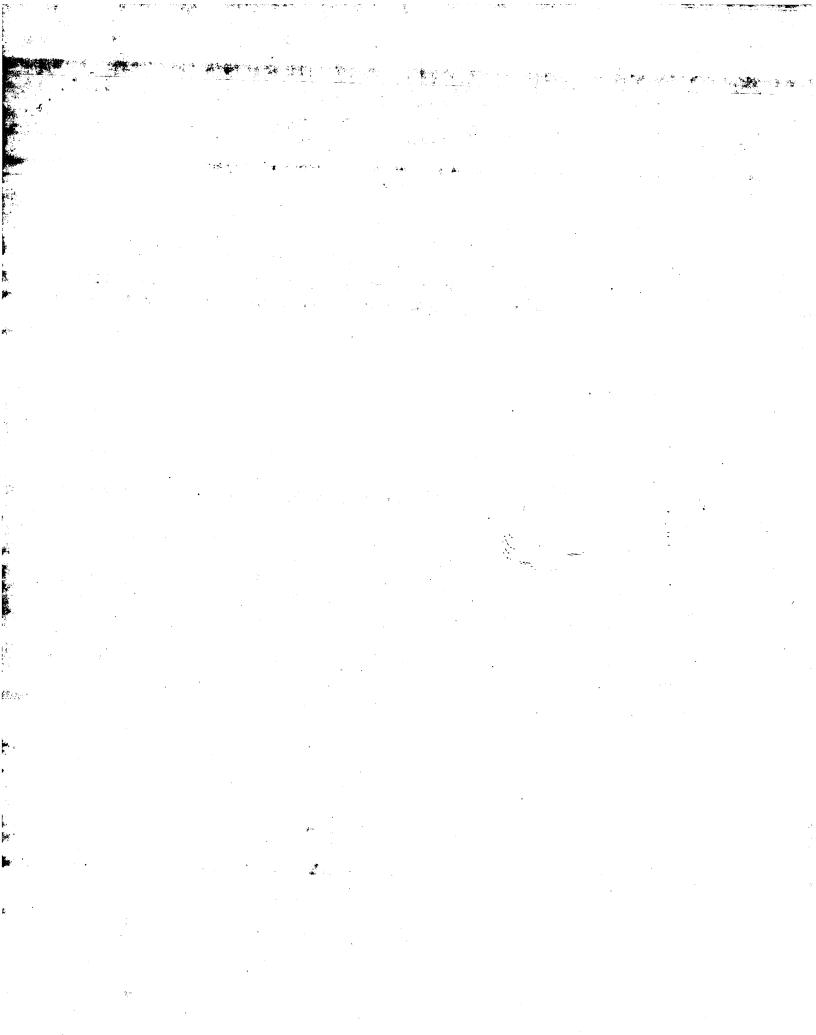
Accession:

Date: 05-Dec-1997

oxaloacetate decarboxylase, biotin carboxyl carrier subunit homolog - Archaeoglobus C; Species: Archaeoglobus fulgidus

#sequence_revision 05-Dec-1997 #text_change 20-Aug-1999

Search completed: May Job time: 20.4271 secs ۲ 2003, 07:50:27



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Post-processing: Minimum Match 0%
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Listing first 100
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Sequence 111784,
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10538, A
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Result No.

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Minimum Maximum

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Searched:

Scoring table:

Title: Perfect score:

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APPLICANT: Barry, Michael
APPLICANT: Parrott, Michael
APPLICANT: Parrott, Michael
FITLE OF INVENTION: Methods for the In Vivo Bic
FILE REFERENCE: 15987/268653
CURRENT APPLICATION NUMBER: US/09/987,485
CURRENT FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 122
TYPE: PRT
                                                                                                                                                            Sequence 5, Application US/09148920 GENERAL INFORMATION:
                         TITLE OF INVENTION: Recombinant Antigen Immunoassay TITLE OF INVENTION: Syphilis FILE REFERENCE: p-4131 CURRENT APPLICATION NUMBER: US/09/148,920 CURRENT FILING DATE: 1997-09-04
                                                                                                                       APPLICANT: Mullenix, Michael C. APPLICANT: Deutsch, John
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLKVTVNGTAYDVDVDVDKSHENPMGTILFGGGTGGAPAPAAGGAGAGKAGEGEIPAPL
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8 US-10-1511-129-337-63783
21 US-09-791-537-6475
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Sequence 1375, Ap
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US-09-191-537-120787
; Sequence 120787, Application US/09791537
; GENERAL INFORMATION:
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US-09-148-920-5
Sequence 7, Application US/10251313

GENERAL INFORMATION:
APPLICANT: AMENOSIUS, DOROTHEE
APPLICANT: LANZENDOERFER, MARTIN
APPLICANT: SCHRAEML, MICHAEL
APPLICANT: WATZELE, MANFRED
TITLE OF INVENTION: IMPROVED METHOD FOR A SEQUENCE SPECIFIC BIOTINYLATION
FILE REPERENCE: 506.1001
CURRENT APPLICATION NUMBER: US/10/251,313
CURRENT FILING DATE: 2002-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/791,537
CUBRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 120787
LENGTH: 129
TYPE: PRT
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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; ORGANISM: Escherichia US-09-987-485-1

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Query Match Best Local (

Similarity

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RESULT 1. US-09-987-485-1

Sequence 1, Application GENERAL INFORMATION:

RESULT 2 US-09-148-920-5

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; OTHER INFORMATION: ; OTHER INFORMATION: US-10-251-313-7
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US-09-148-920-7
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US-09-148-920-3
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Sequence 7, Application US/09148920 GENERAL INFORMATION: APPLICANT: Mullenix, Michael C.
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CURRENT FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mullenix, Michael C.
APPLICANT: Deutsch, John
TITLE OF INVENTION: Recombinant Antigen Immunoassay for the Diagnosis
TITLE OF INVENTION: Syphilis
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NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                           LENGTH: 256
TYPE: PRT
ORGANISM: Treponema pallidum
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 8.6e-52;
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Pred. No. 2e-51;
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US-09-791-537-132235
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US-10-251-313-1
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Sequence 1, Application US/10251313
GENERAL INFORMATION:
APPLICANT: AMBROSIUS, DOROTHEE
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Best Local :
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GENERAL INFORMATION
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/148,920 CURRENT FILING DATE: 1997-09-04 NUMBER OF SEQ ID NOS: 7
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TITLE OF INVENTION:
FILE REFERENCE: p-41
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TYPE: PRT
ORGANISM: Treponema
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Pred. No. 8.2e-51;
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Pred. No. 2.1e-51;
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Best Local :
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBITILE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
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TITLE OF INVENTION: IMPROVED METHOD FOR A SEQUENCE SPECIFIC BIOTINYLATION
FILE REFERENCE: 506.1001
CURRENT APPLICATION NUMBER: US/10/251,313
CURRENT FILING DATE: 2002-09-20
CURRENT FILING DATE: 2002-09-20
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                                                                                                                                                                                                                                                                          LENGTH:
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                    106 VKERDAVQGGQGLIKIG 122
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                                                                                          46 AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVL 105
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 VKERDAVQGGQGLIKIG
                                                                     AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVL 60
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                                                                                                                                                                 Similarity
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                                                                                                                                            Conservative
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ilarity 99.2%;
Conservative
                                                                                                                                                               61.3%;
77
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Pred. No. 7.4e-29;
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Pred. No. 8.2e-51;
0; Mismatches 0;
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US-09-791-537-111788
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US-09-987-485-2
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 111788
LENGTH: 145
TYPE: PRT
                                                                                                                                                                                                                            Query Match
Best Local (
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Best Local Similarity
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APPLICANT: Danzer, JOseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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TITLE OF INVENTION: Methods for the In Vivo
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CURRENT FILING DATE: 2001-11-14
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121
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                                                                                                                                                                    1 MKLKVTVNGTAYDVDVD-------VDKSHE------NPMGTILFGGGTGGAPA 40
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                                DGKVEKVLVKERDAVQGGQGLIKIG 122
                                                                                                PA---AGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPT 97
                                                                                                                                  MKVKVVVNGKEYEVDVEEVMPGKFRVTLEGKTYEVEANLGIQVAPVQTQVATPAPTPTPT 60
DGVVKRILVKEGDAVDTGTPLIELG 145
                                                                  PTPVQAPTTPQVQASENVVTAPMPGKVLKILVQEGQQVKLGQGLLILEAMKMENEIPAPR 120
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Pred. No. 1.7e-25;
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Pred. No. 2.8e-14;
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RESULT 12
US-09-791-537-111800
; Sequence 111800, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.

APPLICANT:

Derek

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US-09-791-537-111800
                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Veillonella parvula US-09-791-537-54812
Sequence 10079, Application US/60360039 GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
TITLE OF INVENTION: METHODS OF USE THEREOF
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TYPE: PRT
                                                                                                            123 DDMVVLG 129
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                                                                                                                                                                                                                                                       KENVTVNGTAYDVEVNEVKAAAPAAAPKAAPAAAPAKAAPAPAPAPAPAAAAAPVPAGAET 62
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; Pred. No. 9.2e-12;
15; Mismatches 56
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Pred. No.
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US-09-791-537-72996
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US-09-540-209B-9732
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LENGTH: 589
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                   GENERAL INFORMATION:
                                   Sequence 72996,
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
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CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
APPLICANT: Bionomix, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 10444
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                                                                                                                                                                                                                                                                                    30 VEVNGTSYKVELD-----KPV----
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                                                                                                                                                                                                                                                                                                                        5 VTVNGTAYDVDVDVDKSHENPMGTILFGGGTGGAPAPAAGGAGKAGEGE------
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51; Conserv
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Hinkle, Gregory J.
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                                     Application US/09791537
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43.28;
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                                                                                                                                                                                                                                                                                                                                                            Score 203.5; DB 1
Pred. No. 1.5e-11;
5; Mismatches 36
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Pred. No. 7.6e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
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APPLICANT: Danzer, TITLE OF INVENTION: TITLE OF INVENTION:

JOSEPH
THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY

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METHODS OF USE THEREOF

APPLICANT:

Debe, Derek

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US-09-791-537-48753; Sequence 48753; Appl; GENERAL INFORMATION:
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US-09-791-537-5404
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US-09-791-537-5404
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APPLICANT: Debe, Deter APPLICANT: Debe, Deter APPLICANT: Danzer, Joseph TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
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Best Local Similarity
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APPLICANT: Denzer, Joseph
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                 APPLICANT: Bionomix, Inc.
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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SOFTWARE: PatentIn version 3.
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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Pred. No. 4.
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                                                                                    OF PROTEIN FAMILIES AND FAMILY MEMB
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Query Match
Best Local Similarity
Watches 49; Conserve
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US-09-791-537-31887
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Best Local Similarity
Matches 50; Conserv
                                                                                                                                           Sequence 112,
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 31887
LENGTH: 655
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APPLICANT: Slater, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                     APPLICANT:
                                                     APPLICANT:
                                                                                                         APPLICANT: Cao, Yongwei
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CURRENT FILING DATE: 2001-02-22
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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APPLICANT: Debe, Der
APPLICANT: Danzer, J
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SOFTWARE: PatentIn version 3
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                                   Goldman, Barry S.
Hinkle, Gregory J.
Slater, Steven C.
                                                                                       Chen, Xianfeng
                                                                                                                                           Application US/60360039
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                   PLANTS FOR PRODUCTION
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US/60/360,039

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US-09-791-537-36890; Sequence 36890; Application US/09791537; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 111780
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GENERAL INFORMATION:
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SEQ ID NO 112
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Best Local Similarity
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/6
CURRENT FILING DATE: 2002-02-21
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
                                      APPLICANT:
APPLICANT:
                                                      APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
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TYPE: PRT
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35.1%; Pred. No. 3e-10;
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                  OF PROTEIN FAMILIES
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US-09-791-537-36890
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US-60-360-039-1263
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LENGTH: 599
TYPE: PRT
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Best Local Similarity 37.5%;
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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Pred. No. 7.3e-09;
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RESULT 25
US-60-360-039-20329
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; SEQ ID NO 1263
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Pyrococcus horikos
US-60-360-039-1263
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US-60-360-039-20329
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NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13831
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SEQ ID NO 20329
LENGTH: 571
TYPE: PRT
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Best Local Similarity
Matches 45; Conserv
                                APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5252)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILLING DATE: 2002-02-21
                                                                                                                                                           APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xiani
APPLICANT: Goldman, Be
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CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
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APPLICANT: Slater, Steven C.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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                                                                                                                                                                                  Chen, Xianfeng
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Pred. No. 7.3e-09;
4; Mismatches 43
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Pred. No. 7.3e-09;
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14349
LENGTH: 574
                                                                                                                                                                                                                                                                RESULT 28
US-60-360-039-15017
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Best Local Similarity
"~+~hes 47; Conserv:
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                         APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfer
APPLICANT: Goldman, Barr
APPLICANT: Hinkle, Greg
APPLICANT: Slater, Stev
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15017
LENGTH: 574
                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                   Sequence 15017
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                                                                   APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
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                                                        CURRENT FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Agrobacterium tumefaciens
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                                                                                                                                                                                          Xianfeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 176.5;
Pred. No. 4e
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Pred. No. 3.7e-08;
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4e-08;
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APPLICANT: Slater, Gregory J.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14608
LENGTH: 575
TYPE: PRT
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US-60-360-039-14608
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; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-60-360-039-11591
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                                                                                                     ; ORGANISM: Agrobacterium tumefaciens US-60-360-039-14608
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Best Local Similarity 43.89
Matches 42; Conservative
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540 AMKMETQIVATRAGKV-RLIVKEGDYLQAGATLIDI 574
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43.8%; Pred. No. 4e-08;
43.8%; Pred. No. 4e-08;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.7%;
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   Score 176.5; DB Pred. No. 4e-08;
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28;
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                                    27;
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CURRENT FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 122
TYPE: PRT
ORGANISM: Escherichia coli
US-09-987-485-1
                                                                                                                                                                                                                                                                                                                                                                       US-09-987-485-2
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US-09-987-485-1
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Best Local Sim
Matches 122;
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APPLICANT: Barry, Michael
APPLICANT: Parrott, Michael
TITLE OF INVENTION: Methods for the In Vivo Biotin Labeling of Polypeptides
                                                  Query Match
Best Local (
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                                                                                                                                                                                                                                           APPLICANT: Barry, Michael
APPLICANT: Parrott, Michael
TITLE OF INVENTION: Methods for the In Vivo Biotin Labeling of Polypeptides
FILE REFERENCE: 15987/268653
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53 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 112
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                                                Similarity
                                    Conservative
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US-10-184-644-515
US-10-184-644-111
US-10-184-634-111
US-10-123-155-423
US-10-184-644-87
                             Score 342; DB 10;
; Pred. No. 1.1e-24;
0; Mismatches 0;
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                                                             Length 70;
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US-10-169-048-16
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SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 134
TYPE: PRT
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Best Local Similarity
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            CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
                                                                                                            APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                APPLICANT:
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CURRENT FILING DATE: 2002-06-24
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APPLICANT: Holden, David William
TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their
FILE REFERENCE: GJE-97
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APPLICATION
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                                                                                                                                                                                                                                                                                                                                    6940, Application US/09738626 ton No. US20020197605A1
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SENOH, AKIHIRO
                                                                                                                                                                                                                             HAYASHI, MIKIRO
OCHIAI, KEIKO
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                                                                                                                                                              IKEDA, MASATO
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NUMBER:
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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-974-973-2
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TYPE: PRT
CORGANISM: COTYNEbacterium glutamicum
US-09-738-626-6940
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Best Local Similarity
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                                                                     APPLICANT: Hanke, Paul D.

APPLICANT: Hanke, Paul D.

TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacterium FILE REFERENCE: 1533.1230001/MAC/RGM
CURRENT APPLICATION NUMBER: US/09/974,973
CURRENT FILING DATE: 2001-10-21
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CURRENT FILING DATE: 2001-10-21
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NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
EQ ID NO 6940
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SOFTWARE: PatentIn
                PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 19
                                                       PRIOR APPLICATION NUMBER: US 60/239,913
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Local Similarity 38.7%;
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44.6%; Pred. No. 7.3
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Pred. No. 6.3
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SEQ ID NO 19
LENGTH: 1140
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Best Local (
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CURRENT FILING DATE: 2001-10-21
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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TYPE: PRT
ORGANISM: Corynebacterium glutamicum
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                                                                                                                    SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                      YOKOI, HARUHIKO
TATEISHI, NAOKO
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OCHIAI, KEIKO
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43.2%;
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Pred. No. 7.
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US-09-815-242-13363
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                  APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                GENERAL INFORMATION:
                                                                                                                                Sequence 13363, Application US/09815242 Patent No. US20020061569A1
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Best Local Similarity
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APPLICANT: Lessard, Philip A.
APPLICANT: Willis, Laura B.
TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum FILE REFERENCE: 1533.0790002
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                          APPLICANT: Haselbeck, Robert
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US 09/220,081
PRIOR FILING DATE: 1998-12-23
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APPLICANT:
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1 Similarity 43.2%;
32; Conservation
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                Wall, Daniel
Trawick, John D.
                                                    Ohlsen, Kari L.
Zyskind, Judith W.
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43.2%; Pred. No. 1.4e-06;
tive 15; Mismatches 26;
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LENGTH: 161
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APPLICANT:
                                                                                                                                             PRIOR APPLICATION NUMBER: 60/191.078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-03-21
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA,011A
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PRIOR FILING DATE: 2000-11-27
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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PRIOR FILING DATE: 2000-05-23
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                                                                                 APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23 APPLICATION NUMBER: 60/253,625
                                        APPLICATION NUMBER: 60/257,931
                                                                  FILING DATE: 2000-11-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/269,308
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Yamamoto, Robert T.
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Zyskind, Judith W.
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Pred. No. 2.5e-07;
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                                                                                                                                                                                                                                             ; ORGANISM: Staphylococcus aureus US-09-815-242-12361
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SEQ ID NO 12361
LENGTH: 1073
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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SEQ ID NO 13615
LENGTH: 161
TYPE: PRT
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NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification of Essential Genes
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                                                                               935 NGETVEIEIDKGKRLIIKLETISEPDENGNRTIYY------
985 VHTNANVKPKADKSNPSHIGAQMPGSVTEVKVSVGETVKANQPLLITEAMKMETTIQAPF 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                  DR APPLICATION NUMBER: 60/242,578
DR FILLING DATE: 2000-10-23
DR APPLICATION NUMBER: 60/253,625
DR FILLING DATE: 2000-11-27
DR APPLICATION NUMBER: 60/257,931
DR FILLING DATE: 2000-12-22
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                                                                                                                                                                                   Local Similarity
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                                    -----AGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPT 97
                                                                                                                      NGTAYDVDVD---
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Zyskind, Judith W.
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Yamamoto, Robert T
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                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                     for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                2001-02-16
                                                                                                                                                             25.4%; Score 156; DB 10; 29.2%; Pred. No. 2.6e-06; ive 21; Mismatches 41;
                                                                                                                        -VDKSHENPMGTILFGGGTGGAPAPAAGGAG----- 47
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                                                                               -AMNGQARRIYIKDEN 984
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US-10-160-501-17
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                         Sequence 17, Application US/10160501 Publication No. US20030059919A1 GENERAL INFORMATION:
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LENGTH: 1147
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APPLICANT:
APPLICANT: Meyers, Rachel E.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: NOVEL HUMAN 39228, 21956, 25856, 22244,
TITLE OF INVENTION: 50250, 55158, 47765, 62088, 50566, AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                               1121 DGVIKQVTVNNGDTIATGDLLIEI 1144
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5. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.4%; Score 156; DB 10; 29.2%; Pred. No. 2.9e-06;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-160-501-17
                                                                                                                                                                                          RESULT 15
                                                                                                      Sequence 166, Applic
Publication No. US20
GENERAL INFORMATION:
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Best Local :
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LENGTH: 725
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
7ITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory TITLE OF INVENTION: System using Mycobacterium Vaccae
                                                                   APPLICANT: Watson, APPLICANT: Tan, Page 1
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                                                                                                                                                                                                                                                                                                                            598 LKCSVNGVASKAKLII----LEN---TIYLFSKEGSIEIDIPVPKYLSSVSSQETQGGPLA 651
                                                                                                                                                                                                                                                                            59 PLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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APPLICATION NUMBER: US 09/860,821
FILING DATE: 2001-05-18
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APPLICATION NUMBER: US 60/205,961
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                                                                Tan, Paul L.
                                                                                                                         Application US/10051643
o. US20020197265A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version 4.0
                                                                                   James D.
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37.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 153; DB 9;
Pred. No. 3.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 725;
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RESULT 17
US-10-051-643-199
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Sequence 199, Application US/10051643 Publication No. US20020197265A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 33; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/880,505
CURRENT FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Methods and Compounds for the TITLE OF INVENTION: of Immunologically-Mediated : FILE REFERENCE: 11000.1007c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR EPLICATION NUMBER: US 09/324,542
PRIOR FILING DATE: 1999-06-02
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APPLICANT: Tan, Pi
APPLICANT: Presti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/996,624 PRIOR FILING DATE: 1997-12-23
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CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER:
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Prestidge, Ros
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                                                                                                                                                                                                                                                                                     24.48;
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                                                                                                                                                                                                                                                                                     Score 150; DB 9;
Pred. No. 6.9e-07;
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Pred. No. 6.9e-07;
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APPLICANT: Watson, APPLICANT: Tan, P.

James

Matches

29;

Conservative

17;

Mismatches

21;

Indels

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Gaps

0;

60 AG AG

115 GQGLIKI 121

1073 QIGATMSGSVLQVLVKRGDKVEKGQPLLITEAMKMETTIEARFAGTVDHIYVEEGEAISS 1132

55 EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQG 114

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; ORGANISM: Enterococcus faecalis US-09-815-242-10806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 24.4%; Score 150; DB 9; Best Local Similarity 46.5%; Pred. No. 1.7e-06; Matches 33; Conservative 10; Mismatches 28
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SEQ ID NO 199
LENGTH: 243
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: US 08/996,624
PRIOR FILING DATE: 1997-12-23
                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10806 LENGTH: 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 208
                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
DEFOR DETITION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/815,242
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                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                           FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/242,578
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Trawick, John D.
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Zyskind, Judith W.
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                                                                                                                                                                                                               2001-02-16
Score 144;
Pred. No.
  1; DB 10;
3.6e-05;
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                 Length 1142;
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US-09-815-242-10922
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US-09-815-242-4962
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SEQ ID NO 4962
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Best Local
Sequence 10922, Application US/09815242 Patent No. US20020061569A1
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                           Local Similarity
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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APPLICATION NUMBER: 60/253,625
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GENERAL

INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

: Haselbeck, Robert : Ohlsen, Kari L. : Zyskind, Judith W. : Wall, Daniel

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US-09-767-479-4
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-03-21
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-02-16
                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/767,479
FILING DATE: 22-Jan-2001
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO 10922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 NEDVVEFGQPLFRV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 ERDAVOGGOGLIKI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 EIPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR APPLICATION NUMBER: 60/206,848
OR FILING DATE: 2000-05-23
OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                           ZIP: 77210
COMPUTER READABLE FORM:
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ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselkorn, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EITSPIVGIVYLQPAPDKENFVKVGDTVKTGDVVCIVEAMKLMNEITATVDGVITEILVN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162
                                                                                                                                                                                                                                       STATE: Texas
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                       CITY: Houston
               APPLICATION NUMBER: 08/468,793
                                                                                                                                                                                                                                                                                                           STREET: P.O. Box 4433
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DATE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.7%; Score 139.5; DB 40.5%; Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                               ACETYL-COA
METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1e-
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     USE
                                                                                                                                                                                                                                                                                                                                                                                                     CARBOXYLASE COMPOSITIONS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
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                                                                                                                                   #1.30
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US-09-767-479-4
                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 10036
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Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10036,
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-815-242-10036
                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                              PRIOR FILING DATE: 2000-11-
                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-0 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
ORGANISM: Escherichia coli
                                     ENGTH: 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 LMNELESEVTGEVVEILVQNGEPVEFNQPLFRL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 METEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 APTPAAAPPAGPLGGEKFLEITAPMVGTFYRAPAPEEPPFVNVGDRIQVGQTVCILEAMK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 APAPAAGGAGAGKAGEG--EIPAPLAGTVSKI-----LVKEGDTVKAGQTVLVLEAMK 88
                                                                                                                                                                                      APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (512) 418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu, H. Howard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (713) 789-2679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: ARCD:152/KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kitchell, Barbara S. REGISTRATION NUMBER: 33,928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto, Robert T
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35.5%;
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Pred. No. 1.8e-05;
""" anatches 35;
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Gaps

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SEQUENCE DESCRIPTION: SEQ ID NO: US-09-767-479-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09767479 Patent No. US20010036654A1 GENERAL INFORMATION:
Query Match 21.1%; Score 129.5; DB 10; Best Local Similarity 30.7%; Pred. No. 9.4e-05; Matches 31; Conservative 22; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                         TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 VNVGDKVKTG-SLIMI 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 MEVPAPFAGTVKEIKVNVGDKVSTGSLIMVFEVAGEAGAAAPAAKQEAAPAAA----PAP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 VKERDAVQGGQGLIKI 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 31.6%;
les 43; Conservation
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                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000 TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:152/KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                 TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US SN 07/956,700 FILING DATE: 02-OCT-1992
APPLICATION NUMBER: CT-7US93/09340 FILING DATE: 30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-Jan-2001 CLASSIFICATION: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Vers
                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/767,479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/468,793
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Pred. No. 0.00035;
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                                        Length 182;
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                                        RESULT 25
US-09-815-242-12062
                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Staphylococcus aureus US-09-815-242-12581
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SEQ ID NO 12581
LENGTH: 154
Sequence 12062, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                123 NEIGAEISGEIVEILVEDGQMVEYGQPLFKV 153
                                                                                                                                                                                                                 70 APKPTSD-----NHKTINAPMVGTFYKSPSPDEEAYVQVGDTVSNETTVCILEAMKLF 122
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                                                                                                                                                                      91 TEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
                                                                                                                                                                                                                                                       38 APAPAAGGAGAGKAGEGEIPAPLAGTVSK-----ILVKEGDTVKAGQTVLVLEAMKME 90
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                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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o. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                                    19.5%; Score 120; DB 10; 35.2%; Pred. No. 0.00058; tive 13; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                             Length 154;
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GENERAL INFORMATION:

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APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W. APPLICANT: Wall, Daniel APPLICANT: Trawick, John D.

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                                                                                                        CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILLING DATE: 1998-03-30
PRIOR FILLING DATE: 1998-03-30
PRIOR FILLING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 1277/97
PRIOR FILLING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILLING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILLING DATE: 1997-04-18
SEQ ID
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Best Local Similarity
SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48,
                                      PRIOR APPLICATION NUMBER: 60/070,488
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12062
                                                                                                                                                                                                                                                                                                                                         APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DEBIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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CURRENT FILING DATE: 2001-03-21
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OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR APPLICATION NUMBER: 60/269,308
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-16
OR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 APAPAAGGAGAG------KAGEGEIPAPLAGT-----VSKILVKEGDTVKAGQTV
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  PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OETTINGER, Thomas RASMUSSEN, Peter Birk
                                                                                                                                                                                                                                                                                                                                                                                                                                             WELDINGH, Karin
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Pred. No. 0.0011;
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PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SOFTWARE: PatentIn ver. 3.0

SEQ ID NO 5917

LENGTH: 675

TYPE: PRT

ORGANISM: Corynebacterium glutamicum
US-09-738-626-5917
RESULT 28
US-09-815-242-11159
; Sequence 11159, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
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US-09-738-626-5917
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Best Local (
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Best Local
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
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TYPE: PRT
                                                                                                                           189
                                                                                                                                                          115 GQGLIKIG 122
                                                                                                                                                                                               129 LGESVTEGTITQWLKAVGDTVEVDEPLLEVSTDKVDTEIPSPVAGTIVEILADEDDTVDV 188
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                                                                                                                                                                                                                                                                                                                                  18.6%; Score 114.5; DB Local Similarity 27.3%; Pred. No. 0.0099; res. 35; Conservative 20. Winner.
                                                                                                                                                                                                                            58 ---APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
G
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                                                                                                                                                                                                                                                                                                   15 DVDVDKSHENPMGTILFGGGTGGAPAPA-------AGGAGAGKAGEGEIP- 57
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                                                                                                                           GAVIARIG 196
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Pred. No. 0.
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nes 25;
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APPLICANT:

Trawick, John D. Zyskind, Judith W

Daniel

Carr, Grant J.

PPLICANT:

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SEQ ID NO 11159
LENGTH: 155
TYPE: PRT
PRIOR APPLICATION NUMBER: US 60/269,944
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 402
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Publication No. US20030044422A1
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Best Local S
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APPLICANT:
APPLICANT:
                                                                                                                            CURRENT APPLICATION NUMBER: US/10/081,051
CURRENT FILING DATE: 2002-02-20
                                                                                                                                                                      TITLE OF INVENTION: Ehrlichia Ruminantium Polypeptides, Antigens, Polynucleotides, TITLE OF INVENTION: Methods of Use FILE REFERENCE: UF-299XC1
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CURRENT FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 AMKMMNRIEADKAGVVKAILINDGNAVEFDEPLIVI 154
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FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
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APPLICATION NUMBER: 60/257,931
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McGuire, Travis C.
Mahan, Suman M.
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Simbi, Bigboy H.
Ganta, Roman R.
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Conservative
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SEQ ID NO 1386
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TYPE: PRT
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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123
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OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
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                                                                        63 APAATPAMEAPAAAEISGHIVRSPMVGTFYRTPSPDAKAFIEVGQKVNVGDTLCIVEAMK 122
                                                                                                         38 APA--PAAGGAGAGKAGEGEIPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMK 88
                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/257,931
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Yamamoto, Robert T.
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Trawick, John D.
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CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 12317
                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                        APPLICANT:
         APPLICANT: Barth, Brenda
APPLICANT: Douglass, John
APPLICANT: DOUGLASS, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514C1
                                                                                                                                        APPLICANT:
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TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
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                                                                                                                                                                                                                                                                                                                   125
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Similarity 73.88;
                                                                                                                            zhang, ru.
Zhang, Siqing
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Ten, Shyian
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Zhang, Siqing
                                                                    Carter, Darrick
                                                                                  Benson, Darin
Jones, Robert
                                                                                                                                                                   Maisonneuve, Jean Francois
                                                                                                                                                                               Persing, David
Bhatia, Ajay
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Bhatia, Ajay
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                                                                                                              Lodes, Michael
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Jones, Robert
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    NUMBER: US/09/978,825
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                                                                                                        Sequence 10079, Application US/10369493 GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
SEQ ID NO 12317
LENGTH: 125
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Best Local :
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CURRENT FILING DATE: 2001-04-20
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es 90; Conserv
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90; Conserv
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US/10/369,493
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Sequence 1317, Application US/10057498
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of
FILE REFERENCE: 210121.514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 13317
LENGTH: 125
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                        61 AGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGGLIK 120
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Pred. No. 1.6e-29;
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Pred. No. 1.6e-29;
9; Mismatches 21;
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                                               PLANTS
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CURRENT FILING DATE: 2003
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2002-02

2003-02-28

us 60/360,039

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LENGTH: 589
; TYPE: PRT
; ORGANISM: magnetite-containing magnetic coccus
US-10-369-493-10079
US-10-282-122A-48959
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                                                                 SEQ ID NO 48959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR NOTICE 2003-02-20
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            ORGANISM: Bacteroides fragilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT:
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                                               LENGTH: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532 ISKIHVSTGQHVNSGDVVLIMEAMKMETEVRSPLSGTVSSINCKEGNVVNVGDILITL 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 VVVNGTAYNVQV---
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                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-05-23
                                                                                                                                                                  FILING DATE: 2001-02-09
                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                    APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                      PPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48959, Application US/10282122#
                                                                                                                                                                                                                                                      ICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                         CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zamudio, Carlo
Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Forsyth, R.
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Trawick, John
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                                                                                                                                                                                                                                                                                                                                           DATE:
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                                                                                                 Application data removed - NOS: 78614
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Robert
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43.2%;
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                                                                                                                                                                                                                                                                                                                      60/230,347
                                                                                                                                                 60/269,308
                                                                                                                                                                                 60/267,636
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Pred. No. 3.1
                                                                                                               See File Wrapper or PALM
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Query Match

33.1%; Score 203.5;

DB 6;

Length 143;

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                                                                                                                             ; ORGANISM: Klebsiella pneumoniae US-10-282-122A-60140
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                                                                                                                                                           SOFTWARE: PatentIn version 3.1
SEQ ID NO 60140
LENCTH: 588
TYPE: PRT
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Matches 51; Conservative
                                                                 Matches
                                                                                Query Match
Best Local
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                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
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 481 VEVEGKAFVVKV---
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                          5 VTVNGTAYDVDVDVSHENPMGTILFGGGTGG-----APAPAAGGAGAGKAGEG-EIP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LING DATE: 2000-09-06
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                                                                              Similarity
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Carr, Grant
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Forsyth, R.
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Malone, Cheryl
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                                                                              31.7%;
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-----SDGGDVSQLTAAAPASAPAAAAPAGAGTPVT 523
                                                                              Score 195;
Pred. No. 1
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                                                               Mismatches
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                                                            DB 6; I
L.9e-08;
les 37;
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                                                                                          Length 588;
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LENGTH: 655
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APPLICANT:
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                                                                    APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
CURRENT FILING DATE: 2003-02-20
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                                PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-03
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B

PRIOR APPLICATION NUMBER: 60/206,848
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49; Conservative
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Slater, Steven C.
Slater, Barry S.
Goldman, Barry S.
Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zamudio, Carlo
Malone, Cheryl
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Forsyth, R.
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                                                                                                                                                                                                                                                                                   Robert
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; TYPE: PRT ; ORGANISM: Campylobacter jejuni US-10-282-122A-54468 .
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Best Local :
                   PRIOK AFFERDATE: 2000-U5-20
PRIOR FILING DATE: 2000-U5-20
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                          PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                 CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                      PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                              PRIOR FILING DATE:
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               APPLICATION NUMBER: 60/230,347
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FILING DATE: 2000-09-09
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Carr, Grant
Carr, Grant
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Malone, Cheryl
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APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27

FILING DATE:

2000-10-23

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RESULT 11
US-10-369-493-20329
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; ORGANISM: Pyrococcus horikoshii
US-10-369-493-1263
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; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77079
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Sequence 20329, Application US/10369493
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
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LENGTH: 571
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Best Local Similarity
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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SOFTWARE: PatentIn version 3.1
EQ ID NO 77079
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                          511 GKVLRVLVRVGDRVRVGQGLLVLEAMKMENEIPSPRDGVVKRILVKEGEAVDTGQPLIEL 570
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Pred. No. 1.4e-07;
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                                                                                                                                                                                                                                                                                                    ; ORGANISM: Pseudomonas fluorescens US-10-369-493-13831
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SEQ ID NO 13831
LENGTH: 1076
TYPE: PRT
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Best Local
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SEQ ID NO 20329
LENGTH: 571
TYPE: PRT
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CURRENT FILING DATE: 2003-02-28
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                                   106 VKERDAVQGGQGLIKI 121
                                                                                                                                                950 IDVHGETYRVDITGVGVKAEGKRHFYLSIDGMPEEVVFEPLNEFVGGGSSKRKQASA---
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VAKGDRVNPGEILIEI 1075
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                                                                                                            AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVL 105
                                                                         -----PGHVSTTMPGNIVDVLVKEGDTVKAGQAVLITEAMKMETEVQAAIAGKVTAIH 1059
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Slater, Steven C.
Goldman, Barry S.
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Pred. No. 6.6e-07;
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RESULT 13 US-10-369-493-14349 ; Sequence 14349, Application US/10369493

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RESULT 15
US-10-369-493-11591
; Sequence 11591, Application US/10369493
; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15017
LENGTH: 574
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Best Local Similarity
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SEQ ID NO 14349
LENGTH: 574
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(55052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
ATRUDDED OF CEN ID NOS: 47374
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APPLICANT:
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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                                                                                                                                              540 AMKMETQIVATRAGKV-RLIVKEGDYLQAGATLIDI 574
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RESULT 17
US-09-134-000C-6221
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US-10-369-493-14608
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Best Local S
Matches 42
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 11591
LENGTH: 575
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SEQ ID NO 14608
LENGTH: 575
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CURRENT FILING DATE: 2003-02-28
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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CURRENT FILING DATE: 2003-02-28
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                                                                                    541 AMKMETQIVATRAGKV-RLIVKEGDYLQAGATLIDI 575
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                                                                                                                           86 AMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
                                                                                                                                                                                        26 MGTILFGGGTGGAPAPAAGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLE 85 :||: || || || || : ||:
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; Pred. No. 6.8e-07
17; Mismatches 2
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Sequence 6221, Application US/09134000C GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

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RESULT 19
US-10-282-122A-67750
; Sequence 67750, Application US/10282122A
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6221
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US-09-134-000C-6221
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 6221
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CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
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SOFTWARE: PatentIn version 3.1
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CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
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Local Similarity 37.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 175.5;
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Pred. No. 1.6e-07;
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US-10-369-493-18634
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                                                                                                                                  GENERAL INFORMATION:
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                                                                         APPLICANT: Cao,
APPLICANT: Hink
APPLICANT: Slat
                                                                                                                                                      Sequence 18634, Application US/10369493
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
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                   INVENTION:
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Carr, Grant
Carr, Robert
                                                   Hinkle, Gregory J. Slater, Steven C. Goldman, Barry S.
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Zamudio, cu.
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                                   Chen, Xianfeng
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 EXPRESSION OF MICROBIAL PROTEINS PLANTS WITH IMPROVED PROPERTIES
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CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2003-

REFERENCE: 38-10(52052)B 100/369,493

2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21

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LENGTH: 610
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                                        Remaining Prior Application data removed – See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
                                                                          PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                    RELING DATE: 2000-09-05
R APPLICATION NUMBER: 60/242,578
R PTITUS DATE: 2000-10-23
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                                                                                           APPLICATION NUMBER: 60/269,308
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Malone, Cheryl
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; ORGANISM: Bacillus anthracis US-10-282-122A-46866
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; TYPE: PRT
; ORGANISM: Legionella pneumophila
US-10-282-122A-61290
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                                                                                                                                 SOFTWARE: PatentIn
SEQ ID NO 46866
                   Query Match
Best Local
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                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                FILING DATE: 2001-02-1
                                                                                                                                                                                                             APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/242,578
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                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/230,347
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   1 Similarity
37; Conserv
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Malone, Cheryl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wall, Daniel
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Zyskind, Jud
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Tho, Robert
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                   28.5%;
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Score 175; DB 6; L
Pred. No. 2.1e-06;
""Amatches 31;
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Pred. No. 9.4e-07;
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TYPE: PRT
; ORGANISM: Corynebacterium thermoaminogenes
US-10-089-057-4
                                                                                                                                                                                       US-10-169-048-16
                                                                                                                                                Sequence 16, Application US/10169048 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: JP11-282716
PRIOR FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: JP11-311147
PRIOR FILING DATE: 1999-11-01
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CURRENT APPLICATION NUMBER: US/1
CURRENT FILING DATE: 2002-04-03
                                 APPLICANT: Holden, David William
TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their Use
                                                                                           APPLICANT:
                                                                                                               APPLICANT:
                                                                                                                          APPLICANT: Clarke, Edna Elizabeth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-089-057-4
CURRENT APPLICATION NUMBER: US/10/169,048
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KURAHASHI, OSAMU
NAKAMATSU, TSUYOSHI
SUGIMOTO, SHINICHI
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                                                                Zhou, Liqing
Shea, Jacqueline Elizabeth
Feldman, Robert Graham
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OSUMI, TSUYOSHI
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AKIYOSHI, NAOKI
NAKAMURA, KANAE
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Best Local Similarity
Matches 47; Conserv
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SEQ ID NO 16
LENGTH: 134
SEQ ID NO 75568
LENGTH: 591
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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TYPE: PRT
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                                SOFTWARE: PatentIn version
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                                               NUMBER OF SEQ ID
                                                                                    PRIOR FILING DATE: 2001-02-1
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APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
                                                                                                  APPLICATION NUMBER:
                                                                                                                                  APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                   FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                               FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
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                                                                                                                                                                                          FILING DATE: 2000-11-27
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Yamamoto, Robert
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Trawick, John
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Zyskind, Jud
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Malone, Cheryl
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                                                   Application data removed NOS: 78614
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US-10-282-122A-76334
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                                                                          Matches
                                                                                          Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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481 VEVEGKAFVVRVS-DGGDISQLTTAV--PAASSAPVQAAAPAGAGT----PVTAPLAGNI 533
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                                    .5 VTVNGTAYDVDVDVSHENPMGTILFGGGTGGAPAPAAGGAGAGKAGEGEIPAPLAGTV 64
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                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/230,347 FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/230,335 FILING DATE: 2000-09-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/253,625
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                                                                                          Similarity
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Malone, Cheryl
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Trawick, John
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40.2%;
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                                                                      Score 173.5; DB 6;
Pred. No. 1.2e-06;
4; Mismatches 49;
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                                                                                                     DB 6;
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Best Local Similarity
Matches 35; Conserv
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SEQ ID NO 1053
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 69598,
                                                                                                                               FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
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                                                   PRIOR FILING DATE:
PRIOR APPLICATION N
                                                                                                   PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
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                                                                                   PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential Genes
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ORGANISM: Methanococcus jannaschii
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                                                APPLICATION NUMBER: 60/230,335
              APPLICATION NUMBER: 60/230,347
                                   FILING DATE:
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Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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Zyskind, Judith
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Pred. No. 1.
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; ORGANISM: Pseudomonas syringae
US-10-282-122A-69598
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 69598
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Best Local Similarity
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DR APPLICATION NUMBER: 60/257,931

DR FILING DATE: 2000-12-22

DR APPLICATION NUMBER: 60/267,636

DR FILING DATE: 2001-02-09

DR APPLICATION NUMBER: 60/269,308

DR APPLICATION NUMBER: 60/269,308

DR FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
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                                                                                               FILING DATE:
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APPLICATION NUMBER: US/10/282,122A
FILING DATE: 2003-02-20
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Trawick, John
Carr, Grant
Yamamoto, Robel
Forsyth, R.
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Zyskind, Judith
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60/267,636
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Best Local Similarity
Thes 35; Conserve
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                                                      SEQ ID NO 43666
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                                                                                                               PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
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ORGANISM: Pseudomonas aeruginosa
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APPLICATION NUMBER: 60/206,848
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PCT-US02-32727-12317
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Best Local
                     NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 12317
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                      APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: US/09/978,825
CURRENT FILING DATE: 2003.01-29
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
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EQ ID NO 12317
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   LENGTH: 125
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Local Similarity 74.3%;
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Barth, Brenda
                                                                                                                                                                                       Benson, Darin
Jones, Robert
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Benson, Darin
Jones, Robert
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Jen, Shylan
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                                                      ; ORGANISM: Pyrococcus horikoshii US-10-369-493-1263
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; ORGANISM: Propioni acnes
US-09-978-825-12317
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Best Local Similarity
~~+~hes 52; Conserve
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LENGTH: 125
TYPE: PRT
                                                                                                          PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1263
LENGTH: 571
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Best Local Similarity
Matches 52; Conserv
Query Match
Best Local Similarity
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH INPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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CURRENT FILING DATE: 2001-04-20
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514
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74.3%;
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Pred. No. 5.2e-23;
7; Mismatches 11
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Pred. No. 5.2e-23;
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 180; DB 6;
No. 1.8e-12;
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US-10-369-493-20329
                                                                   ; ORGANISM: Aquifex aeolicus US-10-369-493-112
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US-10-369-493-20329
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Best Local S
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                                 Query Match
 Best Local
Matches
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                                                                                                             PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
EQ ID NO 112
LENGTH: 655
                                                                                                                                                                                                 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 CURRENT FILING DATE: 2003-02-28
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TYPE: PRT
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 Similarity 50.0
34; Conservative
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Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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               50.9%;
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               Score 174;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-03-21
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                                                                 1081 ISATMPGTVIKVVVKEGDEVKKGDSMAITEAMKMETTVQAPFNGKVKKVYVNDGDAIQTG 1140
1141 DLLIEL 1146
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                                                                                                                                     Local Similarity hes 35; Conserv
                                64 QGLIKI 69
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                                                                                     4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
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                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/269,308
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Carr, Grant
Carr, Grant
Caroto, Robert
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Malone, Cheryl
Haselbeck, Robert
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                                                                                                                                       13;
                                                                                                                                 Score 174; DB b; red. No. 2.2e-11; rematches 18;
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SEQ ID NO 1053
LENGTH: 567
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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CURRENT APPLICATION NUMBER: US/10/282,122A,
CURRENT FILING DATE: 2003-02-20
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                           PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                       PRIOR FILING DATE: 2000-09-06 PRIOR APPLICATION NUMBER: 60/
                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26
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                                                                                                                                    PRIOR FILING DATE: 2000-09-09
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                                                         FILING DATE: 2000-11-27
                                                                           APPLICATION NUMBER: 60/253,625
                    FILING DATE:
                                    APPLICATION NUMBER: 60/257,931
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Carr, Robert
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Trawick, John
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Malone, Cheryl
Haselbeck, Robert
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    NUMBER:
                    2000-12-22
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60/267,636
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RESULT 11
US-10-282-122A-52088
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HENGTH: 1076
TYPE: PRT
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Best Local S
Matches 35
                                                                   Sequence 52088, Application US/10282122A GENERAL INFORMATION:
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LENGTH: 143
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Best Local :
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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SOFTWARE: PatentIn version 3.1
 APPLICANT:
                                                  APPLICANT:
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CURRENT FILING DATE: 2003-02-28
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                   APPLICANT:
                                   PPLICANT:
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35; Conserva
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                                                  Wang, Liangsu
          Zamudio, Carlo
Malone, Cheryl
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Haselbeck,
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                                   Carlos
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 Robert
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Pred. No. 1.3e-10;
10; Mismatches 23;
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Pred. No. 2.3e-12;
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APPLICANT: APPLICANT: APPLICANT:

> Ohlsen, Kari Zyskind, Judith

Wall, Daniel Trawick, John Carr, Grant

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; TYPE: PRT ; ORGANISM: Clostridium acetobutylicum US-10-282-122A-52088
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                                                                   TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: ELITA 034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
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APPLICANT:
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                PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-0: PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23
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Zyskind, Judith
                                                                                                                                                  Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                        Carr, Grant
                                                                                                                                                                                                         Trawick, John
                                                                                                                                                                                                                             Wall
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Malone, Cheryl
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2000-03-21
NUMBER: 60/206,848
2000-05-23
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50.7%;
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Pred. No. 1.4e-10;
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                                                                                                                     Microorganisms
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; TYPE: PRT ; ORGANISM: Legionella pneumophila US-10-282-122A-61290
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US-10-282-122A-60140
; Sequence 60140, Application US/10282122A
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Best Local :
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                                                                                                                      PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
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PRIOR FILING DATE: 2001-02-09
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                                                   PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                     INVENTION: Identification of Essential Genes
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                                                                                                                                                                                                                                                                                                                                                                       Carr, Grant
Yamamoto, Robert
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Malone, Cheryl
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60/257,931
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Pred. No. 7.8e-11;
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APPLICATION NUMBER: 60/267,636

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                                 SOFTWARE: Pater
SEQ ID NO 77079
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Best Local
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                                                                      Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TYPE: PRT
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                                                                                                                                                          FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
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Zamudio, ca-
Zame, Cheryl
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Yamamoto, Robert
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Pred. No. 1e-10;
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                                                                                     See File Wrapper or PALM
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US-10-282-122A-54468
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                                                                                    Query Match
Best Local Similarity
                                                                        Matches
                                                                                                                                                                                                                    SEQ ID NO 54468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
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                                                                                                                                                                               TYPE: PRT
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529 ENEVLAGISGNVFKIYVNEGEEVKSGQAIMVLEAMKMEIEVNAPKDGIILELCIKIGDTV 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  591 ASLLSL 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     531 VAAPLAGTIFKIQVEQGDEVAEGDVLIVLEAMKMETEIRAARSGVIQELHVKEGDSVRVG 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 QGLIKI 69
                1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60, FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-12-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-09-06
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                                                                                                                                                                                                                                                                                                                           LING DATE: 2001-02-09
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Carr, Grant
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Carr, Grant
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Zamudio, car
Zamudio, car
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Trawick, John
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Zyskind, Judith
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Forsyth, R.
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                                                                      Conservative
                                                                                                                                                                                                                                                                   Application data removed - See File Wrapper or PALM.
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                                                                                     47.78; 50.08;
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                                                                      13;
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                                                                 Score 163; DB 6;
Pred. No. 1.8e-10;
13; Mismatches 20;
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Pred. No. 1.3e-10;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2001-08
                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677, TITLE OF INVENTION: 26320, 46619, 33166, 16836, 46867, 21617, TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 32229, TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR
                                                                                                                                                                                                                                                     CURRENT FILING DATE:
                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/370,959
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                   APPLICATION NUMBER: US 09/715,479
FILING DATE: 2000-11-17
APPLICATION NUMBER: US 60/218,053
FILING DATE: 2000-07-13
                                                                                                                                           FILING DATE: 2000-07-18
APPLICATION NUMBER: US 10/251,507
                                                                                                                                                               APPLICATION NUMBER: US 60/219,028
FILING DATE: 2000-07-18
                                                                                                                                                                                                           APPLICATION NUMBER: US 09/910,150 FILING DATE: 2001-07-18
                                                                                                                         FILING DATE: 2002-09-20
               APPLICATION NUMBER: US 09/644,929
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                                                                                                                                                                                                                                                                                                                                                                                                                    Rudolph-Owen, Laura
Bandaru, Rajasekhar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MacBeth, Kyle J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10370959
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Pred: No. 2.1e-11;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/377,097
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 09/910,150
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                                                                                       PRIOR
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/219,028
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/715,479 FILING DATE: 2000-11-17
                                                                                                      FILING DATE: 2001-06-26
                                                                                                                                                                           APPLICATION NUMBER: US 09/644,929 FILING DATE: 2000-08-23
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37; Conserv
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                                                                                                                                                                                                                                                                                                 G DATE: 2000-07-18
CATION NUMBER: US 10/251,507
                                                                                                                                                                                                                               CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kapeller-Libermann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bandaru, Rajasekhar
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Application data removed NOS: 156
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                                                                                                                   2000-06-16
NUMBER: US 09/892,870
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62088, 46745, 23155, 21657, 42755
32252 MOLECULES AND USES THEREFOR
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                                                                                   US 60/214,174
                                                                                                                                                         us 60/212,439
                                                                                                                                                                                                                               US 60/218,053
                                                  US 09/775,117
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Pred. No. 2.1e-11
1; Mismatches 1
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              See File Wrapper or PALM
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42755, 32229,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55562,
22325,
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; ORGANISM: Pseudomonas syringae US-10-282-122A-69598
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                 Query Match
                                                                                                                SOFTWARE: Pater
SEQ ID NO 69598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ
SEQ ID NO 133
Best Local Similarity
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                                                                                                                                                     Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                        PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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les 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EIKSPMIGESVKEGTPVAEVLVKVGDKVKAGQVLCEVEAMKMEMEIPAPVAGVVKEILVK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGDTVEVGDPLAKI 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                  PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang, Liangsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trawick, John
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Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                          2000-09-09
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                                                                                                                                                                                                                                                                                       2000-11-27
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46.8%;
48.5%;
Score 160;
Pred. No.
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Pred. No. 2.1e-11;
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4e-10;
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            Length 602;
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PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15017
LENGTH: 574
TYPE: PRI
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PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14349

LENGTH: 5740

ORGANISM: Agrobacterium tumefaciens
ORGANISM: Agrobacterium tumefaciens
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                                                                           ; ORGANISM: Agrobacterium tumefaciens US-10-369-493-15017
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Query Match 46.0
Best Local Similarity 50.7
Matches 35; Conservative
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CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                   TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              507 EGEMTAPVSGTLQSFKVKDGETVSEGDLLAVMEAMKMETQIVATRAGKV-RLIVKEGDYL 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QGGQGLIKI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 GGQGLIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
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                                                                                                                                                                                                                                                                                                                          Hinkle, Gregory J.
Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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                                                                                                                                                                                                                                                                                                                                                                                                        Yongwei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.6%; Score 159.5; DB 6 50.7%; Pred. No. 4.2e-10; tive 13; Mismatches 20
46.6%; Score 159.5; DB 6; 50.7%; Pred. No. 4.2e-10; tive 13; Mismatches 20;
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                                     Length 574;
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Gaps
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; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11591
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                                                                          : ORGANISM: Agrobacterium tumefaciens US-10-369-493-14608
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                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14608
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Best Local
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                                    Query Match
Matches
                    Best Local Similarity
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEO ID NOS: 47374
EQ ID NO 11591
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CURRENT FILING DATE: 2003-02-28
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2003-
                                                                                                                                                                                                                                                                                                                                                                                                                            ENERAL INFORMATION:
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                                                                                                                              LENGTH: 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          567 QAGATLIDI 575
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Conservative
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                  46.6%; Score 159.5; DB 6 50.7%; Pred. No. 4.3e-10;
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13;
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Pred. No. 4.3e-10;
13; Mismatches 20;
Mismatches
                                    DB 6;
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                                                                                                                            Query Match
                                                                                                                                                                                                                                                      SEQ ID NO 67750
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 78614 SOFTWARE: Patentin version
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PRIOR APPLICATION NUMBER: 60/
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                                                                                                                                                                                                                       LENGTH: 60
TYPE: PRT
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PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                        ORGANISM: Pseudomonas
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593 PGEILIEI 600
                                                              533 GHVSTTMPGNIVDVLVKEGDMVKAGQAVLITEAMKMETEVQAAIAGKVVAIHVAKGDRVT 592
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                               62 GGQGLIKI 69
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                                                                             GEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQ 61
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Zamudio, cu-
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Zyskind, Jud
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Pred. No. 5.2e-10;
                                                                                                                           Mismatches
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RESULT 25 US-10-282-122A-43666

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                                                                                                                                                                Sequence 19134, Application US/10366683 GENERAL INFORMATION:
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                                  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: PATH03-04
                                                                                          APPLICANT:
                                                                                                                            APPLICANT: Rubenfield, Marc J. APPLICANT: Nolling, Jork
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CURRENT FILING DATE: 2003-02-20
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APPLICATION NUMBER: US/10/366,683 FILING DATE: 2003-02-13
                                                                                          Deloughery, Craig
Bush, David
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Malone, Cheryl
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Forsyth, R.
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Trawick, John
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LENGTH: 612
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PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19134
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                          Sequence 60488, Application US/10282122A GENERAL INFORMATION:
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Best Local Similarity
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                                                                     APPLICANT:
                                                                                                                       APPLICANT:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS
                                                                                                        APPLICANT
                                                                                                                                         APPLICANT:
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                                  APPLICANT
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     Trawit....
Carr, Grant
Carr, Grant
Carr, Grant
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                                                                                                                   Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Yamamoto, Forsyth, R.
                                                                 Wall, Daniel
                                                                                  Zyskind, Judith
                                                                                                      Ohlsen, Kari
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Pred. No. 6.9e-10;
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                                                                           ; ORGANISM: Bacillus halodurans US-10-369-493-17338
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                                                                                                                           NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17338
LENGTH: 1150
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Best Local :
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   Best Local Similarity 50.
                                                                                                                                                                       CURRENT FILING DATE: 2003-
                                                                                                                                                                                                                                                  APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
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                                                                                                               TYPE: PRT
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US-10-282-122a-53885
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LENGTH: 1141
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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1133 GGDLLLVI 1140
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                              62 GGQGLIKI 69
                                                                                                                                              Local Similarity
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Forsyth, R.
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US-09-791-537-111780

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US-09-791-537-111780

US-09-791-537-111780

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US-09-791-537-111790

US-09-791-537-111791

US-09-791-537-111793

US-09-791-537-111794

US-09-791
Sequence 120787
Sequence 3, App
Sequence 111788
Sequence 111788
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Sequence 111780
Sequence 111781
Sequence 11733
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Sequence 115017,
Sequence 116044,
Sequence 11783,
Sequence 2402,
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 2 5468, Ap
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20 23, Appli
20 7481, Ap
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19 Appli

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31867, A
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24359, A
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US-09-987-485-2
Sequence 49119, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: DESCH, JOSEPH
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
LENGTH: 77
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Best Local S
Matches 70
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GENERAL INFORMATION:
APPLICANT: Barry, Michael
APPLICANT: Parrott, Michael
APPLICANT: Parrott, Michael
TITLE OF INVENTION: Methods for the In Vivo Biotin Labeling
FILE REFERENCE: 15987/268653
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CURRENT FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 70
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Local Similarity 100.0%;
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15 US-09-180-505-166
25 US-09-180-625-166
26 US-10-051-643-166
27 US-09-134-000-6221
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20 US-09-152-069A-198
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20 US-09-815-242-13615
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24 US-10-072-851-13615
25 US-10-072-851-13615
26 US-10-072-851-13615
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28 US-09-175-073-3633
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Pred. No. 2.7e-34;
); Mismatches 0;
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APPLICANT: Barry, Michael
APPLICANT: Barry, Michael
TITLE OF INVENTION: Methods for the In Vivo Biotin Labeling of
FILE REFERENCE: 1597/268653
CURRENT APPLICATION NUMBER: US/09/987,485
CURRENT FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 122
TYPE: PRT
ORGANISM: Escherichia coli
US-09-987-485-1
                                                                                                                                  ; ORGANISM: Propionibacterium freudenreichii subsp
US-09-791-537-132235
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Best Local Similarity
Watches 70; Conserve
                                                                                                                                                                                             SEQ ID NO 132235
LENGTH: 123
TYPE: PRT
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APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek APPLICANT: Danzer, Josephapplicant, Josepha
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Matches 70; Conserv
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                             Query Match
Best Local
      Matches
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DADZET, JOSEPH TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 261/210
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   l Similarity
70; Conserv
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Pred. No. 3.1e-34;
0; Mismatches 0;
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DB 21;
5.9e-34;
ss 0;
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US-10-251-313-1
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                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/148,920 CURRENT FILING DATE: 1997-09-04
                                                                                                                                                                                                                                                                                 APPLICANT: Mullenix, Michael C.
APPLICANT: Deutsch, John
TITLE OF INVENTION: Recombinant Antigen Immunoassay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
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CURRENT FILING DATE: 2002-09-20
                                                                                                                                                                                    SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                         ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: EP 01129681.1 PRIOR FILING DATE: 2001-12-13
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                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                       FILE REFERENCE: p-4131
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                                                                                                           TYPE: PRT
ORGANISM: Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                   ITLE OF INVENTION:
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ITLE OF INVENTION: IMPROVED METHOD FOR A SEQUENCE SPECIFIC BIOTINYLATION
ILE REFERENCE: 506.1001
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                                                                                                                                                   ENGTH: 126
                                                                                                                                                                    ID NO 5
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                                                 Local
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                                                 Similarity
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                                   Conservative
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Pred. No. 5.9e-34;
; Mismatches 0;
                               Score 342; DB 15;
Pred. No. 6.2e-34;
Mismatches 0;
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; ORGANISM: Cloning vector PinPoint US-09-791-537-120787
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SEQ ID NO 120787
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Best Local Similarity
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                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: EP 01129681.1 PRIOR FILING DATE: 2001-12-13 PRIOR APPLICATION NUMBER: EP 01122554.7
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CURRENT FILING DATE: 2002-09-20
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
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TYPE: PRT
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NUMBER OF SEQ ID NOS: 153055
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                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: IMPROVED METHOD FOR A SEQUENCE SPECIFIC BIOTINYLATION
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: AMBROSIUS, DOROTHEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bionomix, Inc.
                                                                                                                 LENGTH: 133
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                               OTHER INFORMATION: OTHER INFORMATION:
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                                                                            Description of Artificial Sequence: PinPoint Biotinylation peptide
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Pred. No. 6.4e-34;
Score 342; DB 26;
Pred. No. 6.6e-34;
Mismatches 0;
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US-09-148-920-3
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SEQ ID NO 3
LENGTH: 256
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APPLICANT: Mullenix, Michael C.
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Best Local Similarity
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Best Local 9
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CURRENT FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mullenix, Michael C. APPLICANT: Deutsch, John
                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Recombinant Antigen Immunoassay
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                                                                                                                                                                                                            LENGTH: 26
TYPE: PRT
                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
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ORGANISM: Treponema pallidum
113
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QGGQGLIKIG 122
                                                        EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 112
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                                                                                                                 Score 342; DB 15;
Pred. No. 1.8e-33;
); Mismatches 0;
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RESULT 11

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RESULT 13
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                                                                      US-09-791-537-31867; Sequence 31867, Application US/09791537; GENERAL INFORMATION:
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US-09-791-537-111800
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US-09-791-537-111788
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Matches 38
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Best Local Similarity
Matches 41; Conserv
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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CURRENT FILING DATE: 2001-02-22
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                  APPLICANT:
                                  APPLICANT:
                                                   APPLICANT: Bionomix, Inc.
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CANT: Danzer, Joseph
OF INVENTION: THREE
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DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
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Pred. No. 1.4e-15;
10; Mismatches 19
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Pred. No. 7.8e-15;
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METHODS OF USE THEREOF

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NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1263
LENGTH: 571
TYPE: PRT
ORGANISM: Pyrococcus horikoshii
US-60-360-039-1263
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US-60-360-039-1263
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                                                                                                                                                                                      Sequence 20329, Appl GENERAL INFORMATION:
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FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
                                                     APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                             APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xiani
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SOFTWARE: PatentIn version 3.0
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CURRENT FILING DATE: 2001-02-22
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APPLICANT: Chen, Xianf
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                                                                                                                                                   Chen, Xianfeng
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Pred. No. 6.8e-13;
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Pred. No. 6.8e-13;
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US-09-791-537-111780
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; ORGANISM: Aquifex aeolicus US-09-791-537-31887
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SEQ ID NO 20329
LENGTH: 571
                                                   SEQ ID NO 31887
LENGTH: 655
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                    CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
                                                                                                                                                          APPLICANT: Danzer, JOSEPH
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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les 35; Conserv
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Pred: No. 1.7e-13;
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US-60-360-039-112
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Best Local Similarity
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SEQ ID NO 112
LENGTH: 655
TYPE: PRT
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Best Local Similarity
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                          FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
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                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                       ENGTH: 984
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les 34; Conserv
4 IPAPLAGTYSKILYKEGDTYKAGQTYLYLEAMKMETEINAPTDGKYEKYLYKERDAYQGG
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Hinkle, Gregory J.
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                                                                   50.9%; Score 174; DB 21; 53.0%; Pred. No. 8.1e-12;
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LENGTH: 567
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SEQ ID NO 46258
LENCTH: 567
TYPE: PRT
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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                                                                         EGAVTSPFRGMVTKIKVKEGDKVKKGDVIVVLEAMKMEHPIESPVEGTVERILIDEGDAV 557
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Goldman, Barry S.
Hinkle, Gregory J.
Slater, Steven C.
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50.7%; Pred. No. 5e-12;
tive 12; Mismatches
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; ORGANISM: B.fragilis
US-09-540-209B-9732
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
                                                                                        GENERAL INFORMATION:
                                                                                                             Sequence 107230, Application US/09791537
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                                                     APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek
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CURRENT FILING DATE: 2001-02-22
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBITILE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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EQ ID NO 9732
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APPLICANT: Danzer, Joseph TITLE OF INVENTION: THREE I
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                                                                                                                                                                                                                                           64 QGLIKI 69
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THREE DIMENSIONAL STRUC
METHODS OF USE THEREOF
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Pred. No. 3.6e-12;
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Pred. No. 9.8e-13;
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SEQ ID NO 13831
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Best Local (
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                                                                                                                                                                                                                              Sequence 72996, Application US/09791537
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3
SEQ ID NO 72996
                                                                                                 APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
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                                                           CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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CURRENT FILING DATE: 2002-02-21
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                        PatentIn version 3.0
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51.5%;
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Pred. No. 6.8e-11;
0; Mismatches 23;
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Pred. No. 3e-11;
2; Mismatches
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                                                       ; ORGANISM: Archaeoglobus fulgidus US-09-791-537-111784
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US-09-791-537-36890
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US-09-791-537-36890
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SOFTWARE: Patentin version 3.0
SEQ ID NO 36890
LENGTH: 599
                   Query Match
                                                                                                         SEQ ID NO 111784
LENGTH: 142
Best Local Similarity
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Best Local Similarity
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APPLICANT: Danzer, JOseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                           CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBITITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                               APPLICANT: Bionomix, Inc.
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47.1%;
50.8%;
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Score 161;
Pred. No. 2.
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Pred. No. 5.2e-11;
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DB 21;
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Best Local Similarity 50...
"Chiches 35; Conservative
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CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14349
LENGTH: 574
TYPE: PRT
                                                                       Query Match
Best Local Similarity
Matches 35; Conserv
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SEQ ID NO 15017
LENGTH: 574
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                                                                                                                                                                                                                                         TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)A CURRENT APPLICATION NUMBER: US/60/360,039 CURRENT FILING DATE: 2002-02-21
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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                                                                                                                                                                               TYPE: PRT
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EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
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                                                                       Conservative
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                                                                   46.6%; Score 159.5; DB 27; 50.7%; Pred. No. 2.4e-10; tive 13; Mismatches 20;
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10 US-09-974-973-1.
10 US-09-974-973-2.
10 US-09-974-973-2.
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10 US-09-815-242-1366.
10 US-09-815-242-10806.
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0 US-09-815-242-13163
0 US-09-815-242-1366
Sequence 2, Appli Sequence 1258, Appli Sequence 148, Appli Sequence 11159, Ap Sequence 11159, Ap Sequence 11159, Ap Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 10329, Ap Sequence 10497, Ap Sequence 129, App Sequence 129, Appli Sequence 129, Appli Sequence 127, App Sequence 127, Appli Sequence 2, Appli Sequence 2, Appli Sequence 128, Appli Sequence 4, Appli Sequence 1188, App Sequence 1188, Appli Sequence 1188, Appli Sequence 6, Appli Sequence 11879, App Sequence 11879, App Sequence 10096, Appli Sequence 10096, Appli Sequence 10096, Appli Sequence 11879, App Sequence 11873, App Sequence 11874, Appli Sequence 11874, Appl
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Post-processing: score and is Pred. d. No. is the number of results predicted by chance to have re greater than or equal to the score of the result being is derived by analysis of the total score distribution. 11111987654321 43210...... Minimum Maximum Listing Published_Applications_AA:* : /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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Result No.

Score

Query Match

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342 342 158.5 158.5 155.5 155.5 145.7 146 144 144 144 144

70 122 1157 1157 1140 1140 1140 1140 1140 107 107 108 108 108 108 1147 108 108 1147 1142 1243 1243

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GENERAL INFORMATION:

APPLICANT: BATTY, Michael

APPLICANT: PAIROIT, Michael

TITLE OF INVENTION: Methods for the In Vivo Biotin Labeling of Polypeptides

FILE REFERENCE: 15987/268653

CURRENT APPLICATION NUMBER: US/09/987,485

CURRENT FILING DATE: 2001-11-14

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 2

LENGTH: 70

TYPE: PAT

ORGANISM: Escherichia coli

US-09-987-485-2
                                                                                                                                      ; SOFTWARE: PatentIn version 3.0
; SEO ID NO 1
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-987-485-1
                                                                                                                                                                                                                                                                                                                                                         US-09-987-485-1
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US-09-987-485-2
                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09987485 Patent No. US20020142355A1 GENERAL INFORMATION:
                                                                                                Query Match
Best Local :
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Best Local
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                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/987,485
CURRENT FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                       APPLICANT: Barry, Michael
APPLICANT: Parrott, Michael
TITLE OF INVENTION: Methods for the In Vivo Biotin Labeling of Polypeptides
FILE REFERENCE: 15987/268653
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                           EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
     QGGQGLIKIG 70
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10 US-09-815-242-12136

10 US-09-925-637-50

10 US-09-815-242-5705

10 US-09-815-242-12464

10 US-09-815-242-12464
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                                                                               Score 342; DB 10;
Pred. No. 2.2e-33;
Nismatches 0;
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Pred. No. 1.1e-33;
); Mismatches 0;
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                                                                                  Indels
                                                                                                        Length 122;
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Sequence 10613, A
Sequence 50, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 5705, Ap
Sequence 5705, Ap
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RESULT 5
US-09-974-973-19
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Best Local
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Application US/09974973

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; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-974-973-4
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; SEQ ID NO 2

; LENGTH: 1157

; TYPE: PRT

; ORGANISM: Corynebacterium glutamicum

US-09-974-973-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Hanke, Paul D.
APPLICANT: Hanke, Paul D.
TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacter
FILE REFERENCE: 1533.1230001/MAC/RGM
CURRENT APPLICATION NUMBER: US/09/974,973
CURRENT FILING DATE: 2001-10-21
CURRENT FILING DATE: 2001-10-21
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APPLICANT: Hanke, Paul D.
APPLICANT: Hanke, Paul D.
TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacter
FILE REFERENCE: 1333.1230001/MAC/RGM
CURRENT APPLICATION NUMBER: US/09/74,973
CURRENT FILING DATE: 2001-10-21
CURRENT FILING DATE: 2001-10-21
CURRENT FILING DATE: 2001-10-21
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.0 SEQ ID NO 4
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Best Local Similarity 46.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/239,913
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 19
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PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 19
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                                           61 QGGQGLIKI 69
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EGGDLIVVV 1156
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Pred. No. 2.3e-10;
L3; Mismatches 23;
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US20020177202A1

APPLICANT: Hanke, Paul D.

INFORMATION:

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                                                                                                                                                                                              ; ORGANISM: Corynebacterium glutamicum US-09-738-626-4265
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US-09-974-973-19
                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7059
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PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/974,973
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                                                                                                                                                                                                                                 TYPE: PRT
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                                                  1072 KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVPAATKV 1130
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URRENT APPLICATION NUMBER: US/09/738,626
URRENT FILING DATE: 2000-12-18
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61 QGGQGLIKI 69
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nes 31; Conserv
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                                                                                   1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 00/159162 FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 99/377484
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1999-12-16
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YOKOI, HARUHIKO
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SENOH, AKIHIRO
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                                                                                                                     45.5%; Score 155.5; DB 9;
44.9%; Pred. No. 5.1e-10;
tive 14; Mismatches 23;
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Pred. No. 5.1e-10;
L4; Mismatches 23;
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                                                                                                            ; ORGANISM: Streptococcus pyogenes US-10-169-048-16
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                                       Matches
                                                                        Query Match
                                                                                                                                                                                  SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/10169048 Publication No. US20030072769A1
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/045,072
CURRENT FILING DATE: 2002-01-15
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                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/GB00/04997
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/169,048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER:
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TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
FILE REFERENCE: 1533.0790002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sinskey, Anthony J.
APPLICANT: Lessard, Philip A.
                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                             CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Clarke,
                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                 ILE REFERENCE:
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IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
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    Application US/10045072
on No. US20030027305A1

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                                                                                                                                                                 134
                                    l Similarity
32; Conserv
                                                                                                                                                                                                     PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                             Feldman, Robert Graham
Holden, David William
                                                                                                                                                                                                                                                                                                                                                                                   Shea, Jacqueline Elizabeth
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                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Edna Elizabeth
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                                                                                                                                                                                                                                                                                                                          Streptococcus Pyogenes Virulence Genes and Proteins And Their
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                                                   43.0%;
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Pred. No. 5.1e-10
                                    Score 147; DB 9;
Pred. No. 3.6e-10;
9; Mismatches 26;
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LENGTH: 1073
TYPE: PRT
                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                     APPLICANT:
       APPLECANT: Xu, H. Howard
FITTLE OF INVENTION: Identification of Essential Genes
FITLE OF INVENTION: Prokaryotes
                                                                                                           APPLICANT:
                                                                                                                                               APPLICANT:
                                                                                                                                                             APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                      64 QGLIKI 69
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FILING DATE: 2000-05-26
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Similarity 47.0%;
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US20020061569A1
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                                               Xu, H. Howard
                                                                     Carr, Grant J.
Yamamoto, Robert T.
                                                                                                       Trawick, John D.
                                                                                                                              Wall,
                                                                                                                                           Ohlsen, Kari L.
Zyskind, Judith W.
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Trawick, John D.
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[ON: Prokaryotes
ELITRA.011A
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Pred. No. 6.4e-09;
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LENGTH: 1147
                                                                                                         Matches
                                                                                                                       Best Local Similarity
                                                                                                                                       Query Match
                                                                                                                                                                                                                                             SEQ ID NO 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 166, Application US/10051643 Publication No. US20020197265A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: of Immunologically-Mediated Diseases o TITLE OF INVENTION: System using Mycobacterium Vaccae
                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US09/156,181 PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 2002-01-18
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CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 08/996,624
                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 11000.1008c2
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                                                                                                                                                                                                           LENGTH: 108
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Watson, James D.
                                                                                                                                                                                         ORGANISM: Mycobacterium vaccae
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64 QGLIKIG 70
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                                                         4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
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                                     VDAPFASSVWKVDVAVGDRVVAGQPLLALEAMKMETVLRAPADGVVTQILVSAGHLVDPG 96
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47.88;
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Pred. No. 6.9e-09;
                                                                                                                       Score 144; DB 9;
Pred. No. 6.2e-10;
                                                                                                     Mismatches
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                                                                                                                                       Length 108;
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; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-880-505-166
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                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT EILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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CURRENT APPLICATION NUMBER: US/09/880,505
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PRIOR FILING DATE: 1999-06-02
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                                                                                                          APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
                                                                        FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                               APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23
                                    APPLICATION NUMBER: 60/269,308
                                                            FILING DATE:
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Prestidge, Ross
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Pred. No. 6.2e-10;
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US-09-815-242-13363
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US-09-815-242-13615
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SEQ ID NO 13363
LENGTH: 161
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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144 LVSNEEMVEFGKGLVRI 160
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FILING DATE: 2000-12-22
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                                                              EGNLVESPLVGVVYLAAGPDKPAFVTVGDSVKKGQTLVIIEAMKVMNEIPAPKDGVVTEI 143
                                                                                             EGE-IPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKV 52
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                             LVKERDAVQGGQGLIKI 69
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Pred. No. 1e-09;
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Pred. No. 1e-09;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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SEQ ID NO 199
LENCTH: 243
TYPE: PRT
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 10806
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APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of
TITLE OF INVENTION: System using Mycobacterium Vaccae
                                                                        PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                   PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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CURRENT ETLING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
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Pred. No. 1.7e-09;
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Best Local S
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APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: NOVEL HUMAN 39228,
TITLE OF INVENTION: 50250, 55158, 4777
TITLE OF INVENTION: MOLECULES AND USES
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   PRIOR FILING DATE:
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PRIOR APPLICATION NUMBER: US 09/870,133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/160,501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 09/870,130
                    APPLICATION NUMBER:
                                       FILING DATE: 2000-08-31
                                                      APPLICATION NUMBER: US 60/229,425
                                                                           FILING DATE: 2001-08-31
                                                                                                                               APPLICATION NUMBER: US 60/218,385
                                                                                                                                                                                    FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                          FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/862,535 FILING DATE: 2001-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/207,640 FILING DATE: 2000-05-26
                                                                                                                                                APPLICATION NUMBER: US FILING DATE: 2001-07-16
                                                                                                                                                                                                     APPLICATION NUMBER: US
                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/870,110 FILING DATE: 2001-05-29
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US
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Pred. No. 1.2e-08;
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88, 50566, AND 48118
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                                                       RESULT 19
US-09-815-242-10922
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GENERAL INF
APPLICANT:
                            Sequence 10922, Application US/09815242 Patent No. US20020061569A1
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Best Local Similarity
Matches 27; Conserv
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EQ ID NO 4962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                56 ERDAVQGGQGLIKI 69
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                                                                                                                                                                                                          3 EIPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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                                                                                                                    NEDVVEFGQPLFRV 160
              INFORMATION
                                                                                                                                                                              EITSPIVGIVYLQPAPDKENFVKVGDTVKTGDVVCIVEAMKLMNEITATVDGVITEILVN 146
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Pred. No. 3.5e
12; Mismatches
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Pred. No. 8.9e-09;
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US-09-767-479-2
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Best Local S
Matches 30
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PRIOR APPLICATION NUMBER: 60/
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Versior
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/767,479
FILING DATE: 22-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 NEDVVEFGQPLFRV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 ERDAVQGGQGLIKI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 EITSPIVGIVYLQPAPDKENFVKVGDTVKTGDVVCIVEAMKLMNEITATVDGVITEILVN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 EIPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 55
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Haselkorn, Robert
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                                                                                                                                                                                        CITY: Houston
STATE: Texas
                                                                                                                                                        COUNTRY: United States of America ZIP: 77210
                                                                                                                                                                                                                         ADDRESSEE: Arnold, Wh
STREET: P.O. Box 4433
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                                                             Version #1.30
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; ORGANISM: Corynebacterium glutamicum US-09-738-626-6940
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6940, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                    SEQ ID NO 6940
LENGTH: 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                           PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 00/159162 PRIOR FILING DATE: 2000-04-07 PRIOR APPLICATION NUMBER: JP 00/280988
                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENERAL INFORMATION
                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 NGEPVEYNQPLMRI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 EVASPMVGTFYRAPAPGEAVFVEVGDRIRQGQTVCIIEAMKLMNEIEADVSGQVIEILVQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 ERDAVQGGQGLIKI 69
                                                                                                                                                         WARE: PatentIn ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 EIPAPLAGTVSK-----ILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:152/KIT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
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APPLICATION NUMBER: 08/468,793
FILING DATE: JUNKNOWND
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-OCT-1992
APPLICATION NUMBER: PCT/US93/09340
FILING DATE: 30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                    IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                           YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                      SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAYASHI, MIKIRO
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     36.8%;
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35.1%; Pred. No. 1.4e-07;
Live 19; Mismatches 22;
   Score 126; DB 9;
Pred. No. 7.2e-07;
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                   Length 591;
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US-09-767-479-4
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US-09-815-242-12581
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LENGTH: 154
TYPE: PRT
                                                                                   Sequence 4, Application US/09767479 Patent No. US20010036654A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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CURRENT FILING DATE: 2001-03-21
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 14110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                585 VVLLEI 590
                                                                                                                                                                                                                           141 GQMVEYGQPLFKV 153
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                                                                                                                                                                                                                                                                                                   81 INAPMYGTFYKSPSPDEEAYYQYGDTYSNETTYCILEAMKLFNEIQAEISGEIVEILVED 140
                                                                                                                                                                                                                                                             57 RDAVQGGQGLIKI 69
                                                                                                                                                                                                                                                                                                                                    4 IPAPLAGTVSK-----ILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKE 56
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 QGLIKI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
APPLICANT: Haselkorn, Robert
Gornicki, Piotr
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND
METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carr, Grant J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              34.9%; Score 119.5; 39.7%; Pred. No. 7.9
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CORRESPONDENCE ADDRESS:

OF SEQUENCES:

ADDRESSEE: Arnold, White & Durkee

P.O. Box 4433

STATE: Texas CITY: Houston

COUNTRY: United States of America

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TOPOLOGY: linear;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-767-479-4
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                                                                                                                                                                                                                                                                                            Sequence 48,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                     APPLICANT:
                CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT FILING DATE: 2001-02-20
                                                                                                                                                                                              APPLICANT:
                                                     APPLICANT: FLORIO, Walter TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS FILE REFERENCE: 670001-2002.1
                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                 APPLICANT:
                                                                                                                                                                                                              PPLICANT: ANDERSEN, Peter
RIOR APPLICATION NUMBER: 09/050,739
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            142 NGEPVEFNQPLFRL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                 56 ERDAVQGGQGLIKI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 EITAPMVGTFYRAPAPEEPPFVNVGDRIQVGQTVCILEAMKLMNELESEVTGEVVEILVQ 141
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                                                                                                                                                                                                                                                                          No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: ARCD:152/KIT TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                      8, Application US/09791171
US20020094336A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US SN 07/956,700 FILING DATE: 02-OCT-1992 APPLICATION NUMBER: PCT/US93/09340 FILING DATE: 30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/468,793 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/767,479 FILING DATE: 22-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 158 amino acids
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                                                                                                                                 ROSENKRANDS, Ide
                                                                                                                                                                     OETTINGER, Thomas
RASMUSSEN, Peter Birk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION DATA:
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Matches 3

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                                                                         ; ORGANISM: Escherichia coli
US-09-815-242-10036
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                                                                                                                           SEQ ID NO 10036
LENGTH: 630
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                                    Query Match
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PRIOR APPLICATION NUMBER: 1277/97
PRIOR FILING DATE: 1997-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                          SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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mes 23; Conserv
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SEQ ID NOS: 173
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Zyskind, Judi
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ilarity 34.0%;
Conservative
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Score 113.5;
Pred. No. 2.4e
9; Mismatches
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Pred. No. 1e-06;
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US-09-815-242-11159
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                                                                 Sequence 11322, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for
SEQ ID NO 11159
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          APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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APPLICATION NUMBER: 60/191,078
APPLING DATE: 2000-03-21
APPLICATOR
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Xu, H. Howard
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Daniel
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Pred. No. 8.3e-05;
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RESULT 28
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                                         ; ORGANISM: Ehrlichia ruminantium (formerly Cowdria ruminantium)
US-10-081-051-16
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US-09-815-242-11322
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LENGTH: 156
    Query Match
                                                                                                                     SEQ ID NO 16
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CURRENT FILING DATE: 2002-02-20
                                                                            LENGTH: 40
TYPE: PRT
                                                                                                                                        SOFTWARE: PatentIn
                                                                                                                                                              NUMBER OF SEQ ID NOS: 117
                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/269,944
PRIOR FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                APPLICANT: McGuire, Travis C.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Ebrlichia Ruminantium Polypeptides, Antigens, Polynucleotides,
TITLE OF INVENTION: Methods of Use
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PRIOR APPLICATION NUMBER: 60/207,727
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CURRENT FILING DATE: 2001-03-21
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                                                                                                     402
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Simbi, Bigboy
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Mwangi, Duncan M.
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Xu, H. Howard
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Matches 22; Conservative
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                                                                                                                                                               Sequence 12062, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                         APPLICANT:
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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TATEISHI, NAOKO
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OCHIAI, KEIKO
                             Xu, H. Howard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
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P71122 corynebacte
Q97fr7 clostridium
Q9htd1 pseudomonas
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09kuhl vibrio chol
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Q8rn09 amycolatops
Q9k9m0 baccillus ha
Q9a6c6 caulobacter
O28194 archaeoglob
Q94419 saccharopol
Q54119 saccharopol
Q54110 saccharopol
Q61212 reponema p
Q9fbc1 streptococc
Q9a743 caulobacter
Q92cw1 listeria mo
Q8y846 listeria mo
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Q8y847 rhizobium l
Q40121 lycopersico
Q52603 sulfolobus
Q99rk64 streptomyce
Q98f27 rhizobium l
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Q8uff6 agrobacteri
Q90125 pasteurella
Q91299 pseudomonas
Q9hes8 aspergillus ha
Q9chf5 lacticococcus
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Q9y2d0 rhizobium m
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Q8y9u5 brucella me
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Q96d7 lactococcus
Q9hg613 brucella me
Q9raf9 haemophilus
Q8x113 pichia angu

Q8xvp4 ralstonia s
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Q54761 synechococc
Q9lb26 rhodospiril
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Q9i7e9 drosophila
Q9i7e9 drosophila
Q9ddtl brachydanio
Q9rad8 clostridium
Q9kwu5 bacillus su
Q9kwu6 bacillus su
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149AA long hypothetical
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PROSITE; PS00188; BIOTIN; UNKNOWN_1.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AJ248285; CAB49799.1; -.
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                                                                                                                                                                                                    DGVVKRILVKEGDAVDTGTPLIELG 145
                                                                                                                                                                                                                               DGKVEKVLVKERDAVQGGQGLIKIG 122
                                                                                                                                                                                                                                                             PTPVQAPTTPQVQASENVVTAPMPGKVLKILVQEGQQVKLGQGLLILEAMKMENEIPAPR
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    Euryarchaeota;
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l methylmalonyl-CoA c
    Thermococci;
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P71538
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Pred. No. 2.4
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    Thermococcales;
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   Thermococcaceae;
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HSSP; P10802; 1:
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 PAPA---AGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINA
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STRAIN-VCI / DSM 3638 / ATCC 43587 / JCM 8422; STRAIN-VCI / DSM 3638 / Robb F.T., Brown J.R.; Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.; "The complete sequence of the Pyrococcus furiosus Submitted (FEB-2002) to the EMBL/GenBank/DDBJ data EMBL; AE010188; AAL80797.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Kawarabayasi Y., Sawada M., Horikawa H., Kosugi H., Hosoyama A., Nagai. Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y. Funahashi T., Tanaka T., Kudohi Y., Yamazaki J., Kushida N., Oguchi Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizawa T., Nakamura Y., Robb F.T., Horikoshi K., "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3."; DNA Res. 5:55-76(1998).
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Methylmalonyl-CoAdecarboxylase gamma chain.
                                                                                                                                                                      SEQUENCE 144 AA;
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Archaea; Euryarchaeota;
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InterPro; IPR000089; Biottin_lipoyl.
Pfam; PF00354; biottin_lipoyl; 1.
PROSITE; PS00188; BIOTIN; UNKNOWN_1
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MKVKIVINGEEYEVEVEEIMPGKFKVTLEGETYEVEAKDLGISTPAPVPQV----PTPTPA
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                                                                                     Conservative
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No. 2.
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K.,
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01-JUN-1998
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Huder J.B., Dimroth P.;
J. Biol. Chem. 0:0-0(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U1-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20, Gamma-cub.....
                                                                                                                     Propionigenium modestum
Bacteria; Fusobacteria;
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-- COFACTOR: BIOTIN (BY SIMILARITY).
EMBL; Z24754; CAA80875.1; --
EMBL; L22208; AAC36823.1; --
HSSP; P02905; 1BDO.
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    SEQUENCE FROM N.A
                                                                                Bacteria; Fusobacteria;
NCBI_TaxID=2333;
                                                                                                                                                                                                                                                                       Methylmalonyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biotin.
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Pfam; PF00364; biotin_lipoyl; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94043308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=8227015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.3%; Score 205; D) 39.4%; Pred. No. 2.80 Live 15; Mismatches
                                                                                                                               Propionigenium
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                        RESULT 6
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ATCC 25085;
MEDLINE-99157555; PubMed-10027965;
MEDLINE-99157555, PubMed-10027965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Methylmalonyl-CoA decarboxylase from Propionigenium modestum: and sequencing of the structural genes and purification of the complex.";
                                                                                                                                                                                                                                                                                                    Acidaminococcus fermentans.

Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Acidaminococcaseae; Acidaminococcus.
                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TREMBLIREL 10, 0
01-MAY-1999 (TREMBLIREL 10, 1
01-MAR-2002 (TREMBLIREL 20, 1
Glutaconyl-CoA decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biotin; Lyase.
SEQUENCE 134 AA;
                                                 PROSITE; PS001
Biotin; Lyase.
                                                                          InterPro; IPR001882; Biotin_attach.
InterPro; IPR001089; Biotin_lipoyl.
InterPro; IPR001859; Ribosomal_P2.
Pfam; PF00364; biotin_lipoyl; 1.
PRINTS; PR00456; RIBOSOMALP2.
                                                                                                                                                                                                                                                                                                                                                                                                                         Q92AA7
                                                                                                                                        -!- COFACTOR: BIOTIN (BY SIMILARITY).
EMBL; AF030576; AAC69172.1; -.
HSSP; P02905; 1BDO.
                                                                                                                                                                                                   Braune A., Bendrat K., Rospert S., Buckel W.;
"The sodium ion translocating glutaconyl-CoA decarboxylase
Acidaminococcus fermentans: cloning and function of the ger
                                                                                                                                                                                                                                                                                                                                                GCDC.
                                                                                                                                                                                                                                                                                                                                                                                                           Q9ZAA7;
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InterPro; IPR00089; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl; 1.
PROSITE; PS00188; BIOTIN; 1.
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HSSP; P02905; 18D0
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MEDLINE=98088990;
                                                                                                                                                                                                                                                                                            NCBI_TaxID=905;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
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ol. Microbiol. 31:473-487(1999)
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                                                                PS00188; BIOTIN;
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                                        13908 MW;
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32.0%;
35.5%;
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                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
e gamma subunit (EC 4.1.1.70).
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 Score 196.5; DB 2
Pred. No. 1.5e-08;
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Pred. No. 9.0
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                                        4546006D4F2F4C6B
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              DB 2;
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              Length 145;
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Matches

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Best Local S
Matches 49
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InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000089; Biotin_like.
InterPro; IPR003379; PYC_OADA.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00436; PMGL-11ke; 1.
Pfam; PF00436; PYC_OADA; 1.
PROSITE; PS00188; BIOTIN; UNKNOWN_1.
           01-JAN-1998
01-JAN-1998
01-MAR-2002
                                                                                                                                                                                                                                                                          Pyruvate;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          067484
067484;
                                           028067;
                                                                                                                                                                                                                                                                                                                                                                                                                     Deckert G., Warren P.V., Gaasterland T., Young W.G., Ler Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay N. Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium
  Methylmalonyl-CoA
                                                       028067
                                                                                                                                                                                                                                                                                                                                                                                         Nature 392:353-358(1998)
EMBL; AE000744; AAC07445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98196666; PubMed-9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Aquificae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=63363;
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                                                                                                                                                                                                       RDAVQGGQGLIKI
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 (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last seq)
(TrEMBLrel. 20, Last annu (TrEMBLrel. 20, Last annu yl-CoA decarboxylase, bio
                                                      PRELIMINARY;
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Pred. No. 2.6e-07;
9; Mismatches 52
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sequence update) annotation update) biotin carboxyl car
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Q99ZL6;
01-JUN-2001
                                                                                                           Strair.
Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/C
SEQUENCE FROM N.A.
STRAIR-SF370 / ATCC 700294 / SEROTYPE M1;
MEDLINE-21192684; PubMed-11296296;
MEDLINE-1192684; PubMed-11296296;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D Primeaux C., Sezate S., Suvorov A.N., Kenton S. Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
                                                                                                                                                      (EC 4.1.1.41).
SPY1176.
                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2002 (TrEMBLrel. 20, Putative methylmalonyl-CoA c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001882; Biotin_attach.
InterPro; IPR001882; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl; 1.
PROSITE; PS00188; BIOTIN; UNKNOWL_1.
Hypothetical protein; Complete proteome.
SEQUENCE 140 AA; 15686 MW; 30B449C45489C14A CRC64;
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                                                                                                     Streptococcaceae;
NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=VC-16 / DSM 4304
MEDLINE=98049343; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reducing archaeon Archaeoglobus Nature 390:364-370(1997).
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Archaea; Euryarchaeota;
Archaeoglobaceae; Archae
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PubMed=9389475;
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35.1%;
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decarboxylase, gamma-subunit
                                                                                                                                                                                                                    Created)
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Pred. No.
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fulgidus.";
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     a S., song
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                                       D.J.,
                           J., Savic
Lai H.S.,
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                                               Matches
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MEDLINE-20150912; PubMed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M
Basham D., Chillingworth T., Davies R.M., Felt
Jagels K., Karlyshev A.V., Moule S., Pallen M.
Jagels K., Karlyshev M.A., Rutherford K.M.,
                                                                                                                 Interpro; IPR001882; Biotin_attach.
Interpro; IPR000089; Biotin_lipoyl.
Interpro; IPR000089; HMGL-like.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00682; HMGL-like; 1.
PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                          -1- COFACTOR: BIOTIN (BY SIMILARITY).
EMBL; AL139076; CAB73190.1; -.
HSSP; P20708; 1GHJ.
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InterPro; IPR000089; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl; 1.
PROSITE; PS00188; BIOTIN; 1.
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                                                                                                         Biotin;
                                                                                                                                                                                                                             reveals hypervariable seq
Nature 403:665-668(2000).
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                                                                                                                                                                                                                                                               Quail M.A., Rajandream M.A., Rutherford Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-NCTC 11168; MEDLINE-20150912;
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                Campylobacter jejuni.
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01-OCT-2000
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KFTVAVNGNKYHVEVSYGFDKDVNVKSVKKVEENK--NIISSNSTSSVDA-
                      KLKVTVNGTAYDVDV-----
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                                               48; Conser
                                                                                             Complete proteome.
E 599 AA; 65833 MW;
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1. Acad. Sci. U.S.A. 98:4658-4663(2001).
TOR: BIOTIN (BY SIMILARITY).
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. 15, Last sequence update)
L. 21, Last annotation update
boxylase B subunit (EC 6.4.1.
                                                                                                                                                                                                                                         sequences.";
                       -----DVDKSHENPMGTILFGGGTGGAPAPAAGGAGAGK 50
                                                 15;
                                                         Score 187.5;
Pred. No. 4.1
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l; Mismatches
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Pred. No. 5.
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                                                        .1e-07;
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RESULT 11
Q9KUH1
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Matches 46
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Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00362; HMGL-11ke; 1.
Pfam; PF02436; PYC_OADA; 1.
TIGRFAMS; TIGR01108; DATORIN; 1.
PROSITE; PS00188; BIOTIN; 1.
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TIGR; VC0550; -.
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058564;
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                                                                                                                                                                                                                                                                Biotin; Complete proteome. SEQUENCE 597 AA; 64795 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "DNA sequence cholerae.";
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STRAIN-EL TOR N16961 / SEROTYPE 01
MEDLINE-20406833; PubMed-10952301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio cholerae.
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InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000891; HMGL-like.
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                                                                                                                                                                      VKVDGVVYDVEV
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21, Last annotation update)
oxaloacetate decarboxylase
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Best Local
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Bacteria; Firmicutes; Bacillus/Clostridium group; Thermoanaerobacteriales; Thermoanaerobacteriaceae;
                                                                                         Complete proteome
                                                                                                                                                                                  Tan H.,
                                                                                                                                                                                                                                            MEDLINE-21992816; PubMed-11997336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Oh
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi
Masuchi Y., Shizuya H., Kikuchi H.;
                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             ACCB2 OR TTE2383.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                        %CBI_TaxID=119072;
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InterPro; IPR000089; Biotin_lipoyl.
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thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
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    Loca1
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                                                                                                       o Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., en Y., Xue Y., Xu Y., Lai X., Huang L., Dong n H., Chen R., Wang J., Yu J., Yang H.; complete sequence of T. tengcongensis genome nome Res. 12:689-700(2002).
BL; AE013180; AAM25522.1; -.
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PF00682; HMGL-like; 1.
PF02436; PYC_OADA; 1.
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                                                                  13437 MW;
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  179.5; DB 16;
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Ohfuku Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almelda N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Chapman P., Levy R., Li M.-J., McClelland E., Palmieri A., Gordon D. Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                           Agrobacterium tumefaciens C58. Science 294:323-2338(2001). EMBL; AE009322; AAL447211; -... EMBL; AE008292; AAK89506.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-21608551;
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                       Complete
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STRAIN-MSB8 / DSM 3109;

MEDLINE-99287316; PubMed-10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Nelson K.E., Clayton R.A., Gill S.R., Nelson W.C., Ketchum K.A.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria fro

genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999).

EMBL, AE001743, AAD35799.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
0xaloacetate decarboxylase alpha-chain.
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STRAIN-CORBY;
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Bacteria; Proteobacteria;
Legionellaceae; Legionella
NCBI_TaxID=446;
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Pfam; PF00364; biotin_lipoyl; 1.
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*An oxaloacetate decarboxylase homologue protein
intracellular survival of Legionella pneumophila.
FEMS Microbiol. Lett. 145:273-279(1996).
                                                                                                         Hacker J.
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C., Lueck P.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.6%; Score 176; 33.6%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermotogales;
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12,
20,
                                                                                                                                                                                                                                                                                                                                                                          gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                      subdivision; Legionellaceae
                                                                                                                                  Di Bevardino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.1e-07;
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                                                                      influences
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                                                                                                                                     Dimroth
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                                                                                                                                                                                                                                                                                                                                                                          group;
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RESULT 17

OPYRDJ

OPYRDJ

AC Q9XBJ

AC Q9XBJ

DT 01-NC

DT 01-NC

DT 01-NC

OX Baci

OX Baci

OX NCBJ

RN [1]

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Best Local
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PROSITE;
Biotin.
                                                                                                                                                                                                               InterPro; IPR003379; PYC_OADA.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF02786; CPSase_L_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus cereus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XBJ1;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9ХВJ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMs;
                                                                          SEQUENCE
                                                                                                                                                TIGRFAMS;
                                                                                                                                                                  PRINTS; PR00098;
                                                                                                                                                                                                    Pfam; PF00682;
                                                                                                                                                                                                                                                                                                                                                                    Microbiology 145:621-631(1999).
EMBL; AJ010111; CAB40604.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Okstad O.A., Hegna I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYCA.
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                                                                                           NON_TER
                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99231848; PubMed=10217496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                            Ligase
                                                                                                                                                                                                                                                                                                                                                 HSSP; P24182; 1DV2
                                                                                                                                                                                                                                                                                                                                                                                                                          Genome organisation
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BL; X99678;
SP; P11961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKVTPGQVLIRV
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PF02436;
                                                                                                                                                                                     PF02436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00364; biotin_lipoyl; PF00682; HMGL-like; 1.
 45;
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                             PS00867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00188; BIOTIN; 1.
PS00165; DEHYDRATASE_SER_THR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000891; HMGL-11ke.
IPR003379; PYC_OADA.
IPR000634; S/T_dehydrtse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Firmicutes;
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                                                                                                                                                TIGR01235;
                                                                                                                                                                                                                                                                                          IPR000901; CPSase.
IPR000891; HMGL-like.
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IPR000089; Biotin_lipoyl.
                                                                          984
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
(Themplered. 21, Last annotation update)
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 Conservative
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; CAA67994.1;
; 1LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,
                                                                          ă,
                                                                                                                                                                               HMGL-like; 1
PYC_OADA; 1.
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                                                                                                                                                                CPSASE.
                                                                                                                           35; pyruv_carbox; 1. CPSASE_2; UNKNOWN_1.
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110135
                   28.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Lindbaeck T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                          MW;
 19;
                                                                                                                                                                                                                                                                                                                                                                                                                        conserved
                   Score 176; DB 2;
Pred. No. 6.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 176; DB 2;
Pred. No. 3.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
Mismatches
                                                                        7AB52F8D453A147D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Rishovd A.L., Nors
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 49;
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                                Length 984;
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 20;
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RESULT QUESTION ACCORD 
RESULT 19
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Best Local :
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InterPro: IPR000089; Blotin_lipoyl.
InterPro: IPR000089; Blotin_lipoyl.
InterPro: IPR0000901; CPSase.
Pfam; PF02785; Blotin_carb_C; 1.
Pfam; PF00289; CPSase_L_bain; 1.
Pfam; PF02786; CPSase_L_D2; 1.
  Q8RQN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Acad. Sci. U.S.A. 97:12176-12181(2000).
HSSP; P24182; IBNC.
Interpro:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; Genome sequence of Halobacterium species NRC-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=20504483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biotin carboxylase. ACC OR VNG1532G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00188; BIOTIN; UNKNOWN_1.
PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=64091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteria;
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InterPro; IPR001882; Biotin_attach.
InterPro; IPR001882; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl; 1.
PROSITE; PS00188; BIOTIN; 1.
Biotin; Complete proteome.
SEQUENCE 132 AA; 13529 MW; 2FA2B1
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01-JUN-2001
01-MAR-2002
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Acvl-CoA carboxylase B and C subunit.
                                                                                                                                                                                                                                                                                                        Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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Hirano S., Kimura E., Kawahara Y., Sugimoto S.;

"accBC of Corynebacterium efficiens.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AB083052; BAB88668.1;

EMBL; AB083052; BAB88668.1;

SEQUENCE 591 AA; 63236 MW; 345BCEC36C5D8ACA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcaceae;
NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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MEDLINE-21192684; PubMed-11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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17, Last sequence up
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                        Score 173.5; DB Pred. No. 9.5e-07
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Pred. No. 4.
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01-MAR-2002 (TrEMBLrel. 21, I
01-JUN-2002 (TrEMBLrel. 21, I
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01-JUN-2002 (TERMBLrel. 21, Last annotation update)
Biotin carboxyl carrier protein of propionyl-CoA carboxylase
subunit (EC 6.4.1.3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-21332296; PubMed-11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard
                                                                            Q8XGX8
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InterPro; IPR00089; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl; 1.
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Archaea; Crenarchaeota;
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                                                                                                                                                                                                           PAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQ 116
                                                                                                                                                                                                                                                                    VNGTAYDVDVDVSHENPMGTILFGGG-----TGGAPAPAAGGAGA-----GKAGEGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------GAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPT
                                                                                                                                           ILIVI
                                                                                                                                                                  GLIKI 121
                                                                                                                                                                                                                                             INGKKYYVFIESD
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                                                                                                                                                                                                                                                                                                                                             Complete proteome.
E 186 AA; 21166 MW;
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                            185
                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                            PRELIMINARY;
                                                                                                                                                                                                                                           -----GTLIFNHODFLRLDKVTEIPIKGEERVEEIIRGK--EGEI 120
                                                                                                                                                                                                                                                                                                       28.2%;
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18,
21,
           20, Created)
20, Last sequence update)
21, Last annotation update
ase alpha chain (EC 4.1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermoprotei;
                                                                                                                                                                                                                                                                                                                                                                        UNKNOWN_1.
                                                                                                                                                                                                                                                                                               14;
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                                                                                                                                                                                                                                                                                                        Score 173.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                               DB26587C39883B08 CRC64;
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                                                                                                                                                                                                                                                                                              Mismatches
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                                                                            591
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              ation update) (EC 4.1.1.3)
                                                                                                                                                                                                                                                                                                         1.4e-06;
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                                                                           B
                                                                                                                                                                                                                                                                                                                     DB 17;
                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                     186;
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RESULT
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Best Local :
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O1-JUN-2002 (TrEMBLrel. 2:

O1-JUN-2002 (TrEMBLrel. 2:

O1-JUN-2002 (TrEMBLrel. 2:

O1-JUN-2002 (TrEMBLrel. 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003379; PYC_OADA.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00682; HMGL-like; 1.
Pfam; PF02436; PYC_OADA; 1.
TIGRFAMS; TIGR01108; oada; 1.
PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.
                   Kapatral V., Anderson I., Ivanova N., Reznik G., Los T
Bhattacharyya A., Bartman A., Gardner W., Grechkin G.,
Vasieva O., Chu L., Kogan V., Chaga O., Goltsman E., Be
Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn
Fonstein M., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of a enterica serovar Typhi CT18."; Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkhill J., Dougan G., James K.D., Thomson N.R., Churcher C., Mungall K.L., Bentley S.D., Holden M. Baker S., Basham D., Brooks K., Chillingworth T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CT18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                        SEQUENCE FROM N.A.
STRAIN-ATCC 25586;
MEDLINE-21886394; PubMed-11889109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21534947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella typhi.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OADA OR STY3532.
nucleatum
                                                                                                                                           rusobacterium nucleatum Bacteria; Fusobacteria; NCBI_TaxID=76856;
                                                                                                                                                                                                             Biotin carboxyl carrier
                                                                                                                                                                                                                                                                                  Q8R5Y8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00188; PROSITE; PS00095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quail M., Rutherford K., Si
Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=601;
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        Genome sequence
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                                                                                                                                                                                                                                                                                                                                                                                                     VEVEGKAFVVRVS-DGGDISQLTTAV--PAASSAPVQAAAPAGAGT----PVTAPLAGNI 533
                                                                                                                                                                                                                                                                                                                                                                                                                            VTVNGTAYDVDVDVDKSHENPMGTILFGGGTGGAPAPAAGGAGAGKAGEGEIPAPLAGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL627278; CAD07867.1;
AL627265; CAD01210.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001882; Biotin_attach.
IPR000089; Biotin_lipoyl.
IPR001525; C5_DNA_meth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA; 63372
and analysis of the oral bacterium Fusobacterium ATCC 25586.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C5_MTASE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=11677608;
an G., James K.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; C5_DNA_meth.
1; HMGL-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.2%;
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                                                                                                                                                          (subsp. nucleatum).
Fusobacterium.
                                                                                                                                                                                                             21, Created)
21, Last sequence update)
21, Last annotation update)
protein of glutaconyl-CoA decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a multiple drug resistant Salmonella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 173.5;
Pred. No. 5.
                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                  134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16;
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M.T.G., Se
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                                                     ST.,
Zhu
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                                                                           Lykidis
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                                                                                                                                                                                                                                                                                                                                                                            121
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Best Local S
Matches 46
                                                                                                                                                                                               Matches
                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC 13032;
STRAIN-ATCC 13032;
MEDLINE-96337861; PubMed-8772169;
MEDLINE-96337861; PubMed-8772169;
Jager W., Peters-Wendisch P.G., Kalinowski J., Puhler A.;
Tager W. Peters-Wendisch P.G., Kalinowski J., Puhler A.;
The Corynebacterium glutamicum gene encoding a two-domain profit of the state of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P71122
P71122;
                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-ATCC 13032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                        478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales;
Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 184:2005-2018(2002).
EMBL; AE010533; AAL94406.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001882; Biotin_attach.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000901; CPSase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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   58 APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                     Local
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                                                                                                    KLKVTVNGTAYDVDVDVDKSHENPMGTILFGGGTGGAPAPA----AGGAGAGKAGEGEIP
                                                                        KVVVEINGRRVEVALPGD-
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PF00364; biotin_lipoyl; 1.
PF00289; CPSase_L_chain; 1.
PF02786; CPSase_L_D2; 1.
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46; Conser
                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                     PS00188; BIOTIN; 1
PS00867; CPSASE_2;
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7 (TrEMBLrel. 02,
2 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                591
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119
                                                                                                                                                                                                                                                                                                                63419 MW;
                                                                                                                                                                                                                     27.7%;
38.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.0%; Score 172; DB 16; 34.8%; Pred. No. 1.3e-06; 34.8%; Pred. No. 52;
                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                     UNKNOWN_1.
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                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                 Score 170.5;
                                                                 --- LALGGTAGPKKKAKKRRAGGAKAGVSGDA-VA
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                                                                                                                                                                                                                                                                                                            OC9ED9DE184F8EF4 CRC64;
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                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                     .3e-06;
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Best Local
Q9HTD1;
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete
SEQUENCE
                                                                                                                                                                                                                                                    1130
                                                                                                                                                                                                                                                                                                                                                                     1070
                                                                                                 Q9HTD1
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Gibson R., Lee
                                                                                                                                                                                                                                                                                                      108
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              527
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InterPro; IPR003379; PYC_OADA.

Pfam; PF02785; Biotin_carb_C; 1.

Pfam; PF00364; biotin_lipoyl; 1.

Pfam; PF00289; CPSase_L_chain; 1.

Pfam; PF00289; CPSase_L_D2; 1.

Pfam; PF00682; HMGL-like; 1.

Pfam; PF02436; PYC_OADA; 1.

PRINTS; PR00098; CPSASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TIGR01235; pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN; UNKNOWN_1.
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00481; POLITIAC; 1.
TIGREAMS; TIGR01235; Pyruv_c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001882; Biotin
InterPro; IPR000089; Biotin
InterPro; IPR000901; CPSase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tatusov R.L., Sabathe F., Doucette-Sta
Bennett G.N., Koonin E.V., Smith D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 824 / DSM 792 / VKM B-
MEDLINE-21359325; PubMed-11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000891; InterPro; IPR003141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyruvate carboxylase, PYKA.
                                                                                                                                                                                                                                                                                48 AGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107
                                                                                                                                                                                                     ERDAVQGGQGLIKI 121
                                                                                                                                                               EGDQVQSGQLLVKL
                                                                                                                                                                                                                                        ADSSNKKEIGASIPGNVVKVFVKPGDKVKKGDSLMVIEAMKMETNVSVSEDGTVGGIFVK 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APMQGTVIKVNVEEGAEVNEGDTVVVLEAMKMENPVKAHKSGTVTGLTVAAGEGVNKGVV 586
                                                                                                                                                                                                                                                                                                                       Similarity
35; Conserv
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1144 AA;
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  (TrEMBLrel.
                                                            PRELIMINARY;
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                                                                                                                                                               1143
                                                                                                                                                                                                                                                                                                                                                                                                      127709 MW;
                                                                                                                                                                                                                                                                                                                                        27.6%;
47.3%;
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16,
Created)
Last sequ
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                                                                                                                                                                                                                                                                                                                     Score 170; DB 16;
Pred. No. 2.2e-05;
3; Mismatches 26;
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                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                      519FA29A8008F326 CRC64;
  sequence update)
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                                                                                                                                                                                                                                                                                                                                                             Length 1144;
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P., Daly M.J.,
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RESULT
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OF OF COMMENT OF
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Matches 44
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InterPro; IPR000891; HMGL-like.
InterPro; IPR000379; PYC_OADA.
InterPro; IPR000634; SyT_dehydrtse.
Pfam; PF00364; blotin_lipoyl; 1.
Pfam; PF00682; HMGL-like; 1.
Pfam; PF02436; PYC_OADA; 1.
                                                                                                                                                                                                                                                                                                                                                                                           O67544 PRELIMINARY; PRT; 620 AA.
O67544;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Oxaloacetate decarboxylase alpha chain.
OADA OR AQ.1614.
Bacteria; Aquificae; Aquificales; Aquificaceae; Aqu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
                                                                       MEDLINE-98196666; PubMed-9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Hube.
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE004956; AAG08820.1; -. HSSP; P02905; 3BDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
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       Nature
                                           aeolicus
                                                   "The complete genome of the aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=63363;
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Best Local S
Matches 47
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InterPro; IPR001882; Biotin_attach.

InterPro; IPR001882; Biotin_attach.

R InterPro; IPR000089; Biotin_lipoyl.

R InterPro; IPR000891; HMGL-like.

R InterPro; IPR003379; PYC_OADA.

R Ffam; PF00364; biotin_lipoyl; 1.

R Pfam; PF00682; HMGL-like; 1.

R Pfam; PF00682; HMGL-like; 1.

R Pfam; PF00436; PYC_OADA; 1.

R PTGRFAMS; TIGR01108; oadA; 1.

R R PROSITE; PS00188; BIOTIN; 1.

R PROSITE; PS00188; BIOTIN; 1.

R PROSITE; PS0018; BIOTIN; 1.

Biotin; GTP-binding; Microtubules; Complete proteome.

SEQUENCE 620 AA; 70416 MW; 4F306D48794AE859 CRC64;
                                                                                          Matches
                                                                                                               Query Match
Best Local
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Chen Y., Xue Y., Xu Y., Lai X., Huang L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis
Genome Res. 12:689-700(2002).
EMBL; AE013084; AAM24452.1; -.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-MB4T / JCM11007;
MEDLINE-21992816; PubMed-11997336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8RAJ2
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-!- SIMILARITY: BELONGS TO THE TUBULL
EMBL, AE000747: AAC07497.1; --
HSSP; P02905; 1BDO
                                                                                                                                                                               EMBL; AE013084; AAN Complete proteome. SEQUENCE 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermoanaerobacter tengcongensis.
Bacteria; FirmLoutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanae;
NCBI_TaxID=119072;
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE
CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE
SIMILARITY).
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30.6%;
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Pred. No. 1.4e
17; Mismatches
                                                                                   Score 168; DB ro;
Pred. No. 2.7e-06;
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ABLE SITE ON THE
THE ALPHA-CHAIN
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Best Loc
Matches
                                                      P96890;
01-MAY-1997
01-MAY-1997
01-MAR-2002
                       01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
BCCA (Acetyl/propionyl-CoA carboxylase, alpha sub
ACCA3 OR RV3285 OR MTCY71.25 OR MT3384.
              Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591786; CAC45899.1; -.
InterPro; IPR001249; ACCOA_biotinCC.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR000889; Biotin_lipoyl.
Pfam; PF000364; biotin_lipoyl; 1.
Pfam; PF000364; biotin_lipoyl; 1.
PROSITE; PS00188; BIOTIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Caddeu E., Dreano S., Gloux ; Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Gailbert F.; *Analysis of the chromosome sequence of the legume symbiont sinorhizobium meliloti strain 1021.*;
 Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable biotin carboxyl carrier protein of acetyl-CoA carboxylase
                                                                                                                P96890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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ACCB OR R01320 OR SMC01344.
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158 AA;
Firmicutes;
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32.8%;
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Pred. No. 3.
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Actinobacteridae
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alpha subunit).
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Biotin; C
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                                                                                                                                                                                                                                                                                                              PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000901; CPSase.

Pfam; PF02785; Biotin_carb_C; 1.

Pfam; PF00364; biotin_lipoyl; 1.

Pfam; PF00289; CPSase_L_chain; 1.

Pfam; PF02786; CPSase_L_D2; 1.
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Cole S.T., Brosch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laboratory strains.
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NCBI_TaxID=1773;
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completed: May ne : 72.7188 sec
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                                                                                   QGLIKI 121
                                                                                                              VTAPMQGTVVKFAVEEGQEVVAGDLVVVLEAMKMENPVTAHKDGTITGLAVEAGAAITQG
                                                                                                                                 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG
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AE007147; AAK4772
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45; Conserv
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393:537-544(1998).
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35.7%;
                                                                                                                                                                                                                                                                                      63782 MW;
              2003,
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              07:52:24
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Pred. No. 2
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.2e-05;
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                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transferase (Transcarboxylase, 1.3S subunit).
Propionibacterium freudenreichii shermanii.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobac Actinomycetales; Propionibacterineae; Propionibacteriaceae; Propionibacterium.
NCBI_TaxID-1752;
                                                       BINDING
                                                                                                                               EMBL; M11738; AAA25674.1; PIR; A03401; BKIP.
                                                                                                                                                                                                                                                                                                                                                                                                               blotin enzyme, mutagenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               Shenoy B.C., Xie Y., Samols D.;
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Ericsson L.H., Walsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-85298212; PubMed-3898065;
Murtif V.L., Bahler C.R., Samols D.;
"Cloning and expression of the 1.3S biotin-containing subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biotin carboxyl carrier protein of methylate)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGENESIS OF ALA-87; MET-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Amino acid sequence of the biotinyl subunit from transcarboxylase.";
J. Biol. Chem. 254:11615-11622(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=80049796; PubMed=40985;
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                                                                                                                                                                                                                                                                                                                                                                                                       Biol.
                                                                                   pro; IPR001882; Biotin_attach.
pro; IPR000089; Biotin_lipoyl.
PF00364; biotin_lipoyl; 1.
                                                                                                                      P02905;
            Similarity
                                                                            PS00188;
                                        89
123
   Conservative
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                                                                            BIOTIN;
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                                          89 E
12367 MW;
            98.3%;
99.2%;
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 Score 604.5;
Pred. No. 5.76
0; Mismatches
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                                                       BIOTIN
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                                           D0980C2065EA9A89 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND MET-90.
            .7e-40;
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                                                                                                                    Query Match
Best Local
                                                                                              Matches
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01-JAN-1990
01-JUL-1993
                                                                                                                                                                                          BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: LYASE AND SODIUM TRANSPORTER.
-1- CATALYTIC ACTIVITY: Oxaloacetate = pyruvate + CO(2).
-1- COFACTOR: BIOTIN AND REQUIRES A SODIUM ION.
-1- SUBUNIT: COMPOSED OF THREE CHAINS (ALPHA, BETA, AND GAMMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schwarz E., Oesterhelt D., Reinke H., Beyreuther K., Dimroth P.; "The sodium ion translocating oxalacetate decarboxylase of Klebsiella pneumoniae. Sequence of the biotin-containing alpha-subunit and
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001882; Blotin_attach.
InterPro; IPR000089; Blotin_lipoyl.
InterPro; IPR000891; HMGI-like.
InterPro; IPR003379; PYC_OADA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J03885; AAA25120.1;
PIR; A28088; A28088.
HSSP; P02905; IA6X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                             Decarboxylase;
                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                            FIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          relationship to other biotin-containing enzymes.";
J. Biol. Chem. 263:9640-9645(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88257085; PubMed=2454915;
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PS00188; BIOTIN; 1
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non-profit institutions as long as its content
and this statement is not removed. Usage by an
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decarboxylase alpha chain
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n (EC
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ies 29;
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StyGene; SG?????; oadA2.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR000089; Biotin_lipoy1.
InterPro; IPR000891; HMGL-like.
InterPro; IPR003379; PYC_OADA.
Pfam; PF00364; biotin_lipoy1; 1.
Pfam; PF00682; HMGL-like; 1.
Decarboxylase;
INIT_MET 0
BINDING 556
SEQUENCE 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-LT2 / SGSC1412 / ATCC //U//20;
MCDLINE-2153948; PubMed-11677609;
MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
MCCLelland M., Forwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Courtney L., Porwollik S., Ali J., Dante M., Grewal N., Mulvaney E.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (Rel. 26, Last
15-JUN-2002 (Rel. 41, Last
Oxaloacetate decarboxylase
(OADA1 OR OADA OR STM0055)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SALTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Woehlke G., Wifling K., Dimroth P.;
"Sequence of the sodium ion pump oxaloacetate
Salmonella typhimurium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q03030;
01-JUL-1993 (Rel.
                                                        TIGRFAMS; TIGRO1108; oada; 1. PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                       StyGene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93054591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: LYASE AND SODIUM TRANSPORTER.

CATALYTIC ACTIVITY: Oxaloacetate - pyruvate + CO(2).

COFACTOR: BIOTIN AND REQUIRES A SODIUM ION.

SUBUNIT: COMPOSED OF THREE CHAINS (ALPHA, BETA, AND GAMMA).
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ng K., Dimroth P.;
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2 OR STM3352).
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Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kitkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Commister genome sequence of the methanogenic archaeon, Methanococcu
                                                                                                                                                                                                                                                                  ATOLINE-21034791; PubMed-11195096;
MEDLINE-21034791; PubMed-11195096;
Mikhopadhyay B., Patel V.J., Wolfe R.S.;
"A stable archaeal pyruvate carboxylase from the hyperthermophi methanococcus jannaschil.";
Arch. Microbiol. 174:406-414(2000).
-i- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Pyruvate carboxylase subunit B (EC 6.4.1.1) (Pyruvic carboxylase
              This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 190-125; 260-270; 277-289; 370-380; 386-409; 422-438; 491-506 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYCB OR MJ1231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanocaldococcaceae;
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                                                                                    PATHWAY: GLUCONEOGENESIS.

PATHWAY: GLUCONEOGENESIS.

SUBUNIT: HETEROOCTAMER OF FOUR
MASS SPECTROMETRY: MW-64160; M
MISCELLANEOUS: ITS OPTIMUM PH
                                                                                                                                                                                                 oxaloacetate.
COFACTOR: ATP,
BICARBONATE.
                                                                                                                                                                                                                                             ATTACHED BIOTIN IN THE FIRST STEP AND GROUP TO PYRUVATE IN THE SECOND.

CATALYTIC ACTIVITY: ATP + pyruvate + F
                                           IS 80-90 DEGREES CELSIUS.
SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES,
AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                   ENZYME REGULATION: INHIBITED EXCEEDED THE ATP ONE, AND BY
SWISS-PROT entry
een the Swiss Ins
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PubMed=8688087;
                                                                                                                                                                                                                MAGNESIUM (OR
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 copyright. It is prod
tute of Bioinformatics
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                                                                                                                        FOUR
                                                                                                                                                                                                                                             pyruvate + HCO(3)(-) = ADP + phosphate
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491-506,
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                                                                                           THE
                                                                                                                                                                                                              COBALT),
                                                            LIPOAMIDE TRANSFERASES
                                                                                                                        SUBUNITS
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AND FUNCTION
                                                                                         OPTIMUM TEMPERATURE
                                                                                                                                                                                                                                                                                                                                                     hyperthermophile
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    collaboration
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01-DEC-1992
01-NOV-1997
                                                                                                                                                                                                         SEQUENCE FROM CONTROL OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                           BCCP_STRMU
P29337;
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                                                                                       modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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HSSP;
                     Pfam;
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ontitles requires a license agreement (See |
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                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                "Biotin-containing protein as a cause of gene probing with streptavidin/biotin.";
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                                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
         Pro; IPR001882; Biotin_attach.
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P02905;
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Multifunctional enzyme; Gluconeogenesis; Magnesium;
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567 AA;
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2; Mismatches
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BIOTIN (BY SIMILARITY).
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16-OCT-2001
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SEQUENCE
                                                                                                                                                                                                                                                                                                           Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Slamnonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith
                                                                                                                                                                                                                         "Massive gene decay in the leprosy Nature 409:1007-1011(2001).
-!- FUNCTION: THIS PROTEIN CARRIES
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Medline-94222829; PubMed-7909542;
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Acetyl-/propionyl-coenzyme A carboxylase alpha cha-
carboxylase (EC 6.3.4.14); Biotin carboxyl carrier
                                                                                                                                                                                                                                                                                             Squares S., S
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Lipid synthesis in mycol carboxyl carrier protein
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Dale J.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 176:2525-2531(1994)
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AND SUBSTRATE SIMILARITY: TO
                                   SUBUNIT: MULTIMER COMPRISED OF 2 DIFFERENT ONE (63/64 kDa) HAS BIOTIN CARBOXYLASE AND FUNCTIONS, WHILE THE SMALLER SUBUNIT POSSES
                                                                 PATHWAY: Long-chain fatty acid biosynthesis; SUBUNIT: MULTIMER COMPRISED OF 2 DIFFERENT SI ONE (63/64 kDa) HAS BIOTIN CARBOXYLASE AND B
                                                                                                                                     COFACTOR: BIOTIN.
                                                                                                                                                     CARRIER PROTEIN AND BIOTIN CARBOXYLTRANSFERASE:
CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier |
- ADP + phosphate + carboxybiotin-carboxyl-carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVOGGOGLIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERD :|||:||:||:|| | | | ::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KFKISIDGKEYLVEMEEISESSVPAATPITPTTENTRAASDQKQQSQTPSPAATASAA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---NTMPAPMPGTILKVLVNVGDTVSENQPLMILEAMKMENEIVAGMAGTVSAIHVSSGQ 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAR-1994)
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130 AA;
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O OTHER B
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                       ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 168;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIOTIN (BY SIMILARITY)

A0D6025EC46FF00B CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.G.,
                                                                                                                                                                                                                           TWO FUNCTIONS:
                                                                                                                                                                                                                                                                        bacillus.";
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                                            POSSESSES
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les 52;
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ENZYMES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        databases
                                                               SUBUNITS, THE BIOTIN CARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain [Includes: Bio
rier protein (BCCP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                         first step.
AND
                                                                                                                                                                                                                         BIOTIN CARBOXYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                            CARBOXYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wheeler P.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the biotin rae and M.
                                                                                                                                                                             protein +
                                                                                                                                                     protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                      LARGER
                                                                                                                                                                             CO(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biotin
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SOFFIFIENCE REPRESENTATION OF THE PROPERTY OF

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001882; Biotin_attach.
InterPro; IPR00089; Biotin_lipoyl.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR0000901; CPSase
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF002785; Biotin_aip_C; 1.
Pfam; PF02786; CPSase_L_D2; 1.
                                                                                                                                                                                                                                                                                                                                                   TSDOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                               Q99MR8; Q9D8R2;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
deficiency.";
J. Clin. Inve
                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
(EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha
subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit)
                             MEDLINE-21102410; PubMed-11181649;
Baumgartner M.R., Almashanu S., Suormala T.,
Packman S., Baumgartner E.R., Valle D.;
"The molecular basis of human 3-methylcroton;
                                                                                             STRAIN-C57BL/6;
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                       MCCC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding;
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                                                                                                                                                                                                                                                                                                                                 MCCA_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481
                                                                                                                                                                                                                                                                                                                                                                                                              540
                                                                                                                                                                                                                                                                                                                                                                                                                                         64 VSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTVNGTAYDVDVDVDKSHENPMGTILFGGGTGGAPAPAAGGAGAGKAGEGE-IPAPLAGT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                            VVKVAVAEGQTVMTGDLVVVLEAMKMENPVTAHKDGIITGLAVEAGTAITQGTVLAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X63470; C2
U00012; AJ
AL583919;
P24182; 11
                                                                                                                                                                                                       OR MCCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR00098:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00188; BIOTIN; 1.
PS00866; CPSASE_1; 1.
PS00867; CPSASE_2; 1.
PS00867; CPSASE_2; 1.
Id blosynthesis; Ligase; Biotin; Multifunctional enzyme;
 Invest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
532
169
299
564
30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA:
                                                                                                                                                                                                                                                                                                                                 STANDARD;
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107:495-504(2001)
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174
299
564
                                                                                                                                                      Rodentia;
                                                                                                                                                                     Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63863 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.5%;
37.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 163; DB 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIOTIN (BY SIMILARITY).
D -> H (IN REF. 1).
; 5F2E291D7C54515D CRC64;
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ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOTIN CARBOXYLASE.
BIOTIN CARBOXYL CARRIER PROTEIN.
                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                             3-methylcrotonyl-CoA carboxylase
                                                                                                                                                                                                                                                                                                                                 717
                                                                                                                                                                                                                                                                                                                                 A
                                                          Obie C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 598;
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                                                            Cole R.N.,
                                                                                                                                                                                                                    subunit)
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Query Match
Best Local
                                          BINDING
DOMAIN
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ACT_SITE
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Arakawa T.,
                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                              MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                     TRANSIT
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밁 Ş 밁 ρ

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Szuki R., Tomita M., Washio T.,
RA Schriml L.M., Staubli F., Szuki R., Tomita M., Washio T.,
RA Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Ra Navashi H., Sato K., Schoenbach C., Seya T., Shibata Y., Storich K.-F.,
RA Saski H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hyushiyaki Y..,
RA Hyushi
                                                                                                                                                                                                                                                                                                                  InterPro; IPR001882; Biotin_attach.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000091; CPSase.
Pfam; PF00289; CPSase.L_chain; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF003785; Biotin_carb_C; 1.
Pfam; PF02786; CPSase_L_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-i-CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3)(-) -
phosphate + 3-methylglutaconyl-CoA.
-i-COFACTOR: Biotin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6J; TISSUE-Pancreas; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF310338; AAG50244.1;
EMBL; AK007782; BAB25253.1;
EMBL; BC021382; AAH21382.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- PATHWAY: Leucine catabolism.
-i- SUBUNIT: Probably a dodecamer composed of six biotin-contai alpha subunits and six beta subunits.
-i- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The European Bioinformatics Institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y.;
"Functional annotation
                                                                                                                                                                                                                                                            tochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:1919289;
  Similarity
                                                                                                                                                                                                                                                                                 PS00867;
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36.0%;
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Score
Pred.
                                                                                                                                    ATP (POTENTIAL).
BY SIMILARITY.
BIOTIN (BY SIMILARITY)
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                                                                                                                     POLY-GLU
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                                                                                                                                                                                                                     METHYLCROTONYL-COA
                                                                                                                                                                                                                                   ; ATP-binding; Transit peptide MITOCHONDRION (POTENTIAL).
                                                           F653FE7AC1E5AA90 CRC64;
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3.3e-05;
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[5]
SEQUENCE FROM N.A.
ISOGAÍ T., Ota T., Hayashi K., Sugiyama T., Otsuki ...
Isogaí T., Ota T., Hayashi K., Sudiyama T., Otsuki S., Yoshikawa Mishikawa T., Nagai K., Sugano S., Aotsuka S., Yamamoto J., Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
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MEDLINE-21295033; PubMed-11401427;
Obata K., Fukuda T., Morishita R., Abe S., Asakawa S., Yamaguchi S., Yoshino M., Ihara K., Murayama K., Shigemoto K., Shimizu N., Kondo I.

"Human biotin-containing subunit of 3-methylcrotonyl-CoA carboxylase gene (MCCA): cDNA sequence, genomic organization, localization to chromosomal band 3q27, and expression.";
Genomics 72:145-152(2001).
                                                                                                                                                                                               Packman S., Baumgartner "The molecular basis of deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O96RQ3: Q9H959; Q9NS97;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
(EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha
subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).
MCCC1 OR MCCA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                      PubMed=11181649;
                                                                                                                                                                                                                                                                                                                                                                                                                                Holzinger A., Roeschinger Kattenfeld T., Thuy L.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21299419; PubMed=11406611;
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Perez-Cerda C., Perez B., Rodriguez-Pombo P., Criado O
Morton D.H., Gibson K.M., Le T.P., Ribes A., Rodriguez
Ugarte M., Penalva M.A.;
"The molecular basis of 3-methylcrotonylglycinuria, a
                                                                                                                                                                                                                                                   Baumgartner
                                                                                                                                                                                                                                                                                                                                                                                          *Cloning of the human
                                                                                                                                                                                                                                                                                                                                                                                                               Roscher A.A.;
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gartner E.R., Va
asis of human 3-
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Nyhan W.L., Ko
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                                                                                                                                                                                                            ., Suormala T., Obie C
Valle D.;
3-methylcrotonyl-CoA
                                                                                  Sugiyama T., Otsuki T., Suzuki Y., S., Aotsuka S., Yoshikawa Y., Y., Saito K., Yamamoto J., Wakamats
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Koch H.G., Muntau A.
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Criado O., Sanz
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mutation;

Polymorphism

ATP-binding; Transit peptide,

209 339 681 538 713

214 339 681 541 718

BIOTIN (BY SIMILARITY).

BY SIMILARITY

ATP

(POTENTIAL).

METHYLCROTONYL-COA MITOCHONDRION

(POTENTIAL)

CARBOXYLASE ALPHA

A -> V (IN MCGI,

MILD FORM).

Similarity

24.98; 37.38;

Conservative

17;

Score 153; DB Pred. No. 9.6e

6e-05; DB 1;

Length 725;

Indels

10;

Gaps

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469 725

469 80433 535 532 464 437 385 325

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в847С6в80606в6С0

CRC64

/FTId=VAR_012791. F -> L (IN REF. 3 AND 4).

/FTId-VAR_012790. S -> F (IN MCGI,

ASYMPTOMATIC SEVERE FORM)

FORM).

/FTId=VAR_012789. /FTId=VAR_012788

-> H (IN MCGI,

AA;

535 532

464 437 385 325 289

R -> S (IN MCGI, /FTId=VAR_012787. L -> P (IN MCGI,

SEVERE SEVERE FORM)

FORM)

/FTId=VAR_012786 /FTId=VAR_012785 M -> R (IN MCGI)

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Pfam; PF00289; CDSase_L_chain; 1
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF02786; CPSase_L_D2; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00867; CPSASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                - PARHWAY: Leucine catabolism.
- SUBUNIT: Probably a dodecamer composed of six biotin alpha subunits and six beta subunits.
- SUBCELLULAR LOCATION: Mitochondrial matrix.
- DISEASE: Defects in MCCC1 are the cause of 3-methylcrotonylglycinuria type I (MCGI, CGA or CG2). recessive disease that is characterized by muscular atrophy, probably of spinal origin.
                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                              EMBL;
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Submitted (MAR
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AF297332;
AF310339;
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BC004214;
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BAA99407.1;
AAK67986.1;
AAG50245.1;
BAB14377.1;
BAB14377.1;
AAH04214.1;
AAH04214.1;
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Biotin_lipoyl.
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PIR; A29271; A29271.
HSSP; P02905; 1BDO.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR001089; Biotin_lipoy1.
Pfam; PP00364; biotin_lipoy1; 1.
PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOffman N.E., Pichersky E., Cashmore A.R.;
"A tomato cDNA encoding a biotin-binding protein.";
Nucleic Acids Res. 15:3928-3928(1987).
-I- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE
CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE
TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA.

TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA.

-I- PATHWAY: Long-chain fatty acid biosynthesis; first step.
-I- SUBCELLULAR LOCATION: Chloroplast.
                                                                                                                                                                                                                                                                                    Fatty acid
NON_TER
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as not removed modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biotin carboxyl carrier protein of acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCCP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYCES
 MCCA_ARATH
Q42523; Q9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon esculentum (Tomato). Eukaryota; Viridiplantae; Strepto
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 Q9SA61;
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D75D018C0BD016BC CRC64;
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Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

A Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

A Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Lunn P., Etgu P., Feldblyum T.V., Feng J.-D., Kan S., Khaykin E.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

A Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Kin C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Kin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

A Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

A Malitscher J., Marzida M., Nguyen M., Nierman W.C., Osborne B.I.,

A Malitscher J. Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Hitchyster W. M., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial p
(EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase a
subunit) (3-methylcrotonyl-CoA; carbon dloxide ligase alpha
MCCA OR ATIG03090 OR F1003_8 OR F1003_9.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant Arabidopsis thallana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weaver L.M., Lebrun L., Franklin A., Huang L., Hot Wurtele E.S., Nikolau B.J.;
"Molecular cloning of the biotinylated subunit of coenzyme A carboxylase of Arabidopsis thaliana.";
Plant Physiol. 107:1013-1014(1995).
                                                                                             -i- PATHWAY: Leucine catabolism.
-i- SUBUNIT: Probably a heterodimer composed of bioti-
alpha subunits and beta subunits (By similarity).
-i- SUBCELLULAR LOCATION: Mitochondrial matrix.
-i- TISSUE SPECIFICITY: In roots, cotyledons, leaves,
                                                                                                                                                                                                   STRAIN-cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs)
SSP consortium (Salk/Stanford/PGEC).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Columbia;
MEDLINE=95232183; PubMed=7716229;
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MEDLINE=20148760; PubMed=10681539;
MCKean A.L., Ke J., Song J., Che F
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MEDLINE-21016719; PubMed-11130712;
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"molecular characterization of the
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                                    beta subunits during
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NEOUS: Temporal and sp
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                                                        of the alpha
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Best Local :
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InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000091; CPSase.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00289; CPSase_L_chain; 2.
Pfam; PF00786; CPSase_L_D2; 2.
                                                                                                                                                                                   027179;
027179;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
15-JUN-2002 (Rel. 41, East annotation
Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubo Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
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ACT_SITE
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                                                                           STRAIN-Delta H;
MEDLINE-98037514; PubMed-9371463;
                                                                                                                                           Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
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                                                                                                                                                                                                                                                                   PYCB_METTH
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EMBL;
EMBL;
HSSP;
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PROSITE; PS00866; CPSASE_1;
PROSITE; PS00867; CPSASE_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion;
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31; Conservative
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MITOCHONDRION (POTENTIAL).

METHYLCROTONYL-COA CARBOXYLASE ALPHA CHAIN.

ATP (POTENTIAL).

BY SIMILARITY).

BY SIMILARITY).

V -> D (IN REF. 1).

A -> AK (IN REF. 1).

M -> L (IN REF. 1).

M -> L (IN REF. 1).
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RESULT 12
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Best Local :
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InterPro; IPR000889; Biotin_lipoy
InterPro; IPR000891; HMGL-like.
InterPro; IPR003379; PYC_OADA.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF000682; HMGL-like; 1.
Pfam; PF02436; PYC_OADA; 1.
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"Purification, regulation, and molecular and biochemical characterization of pyruvate carboxylase from Methanobac' thermoautotrophicum strain deltaH.";
J. Blol. Chem. 273:5155-5166(1998).
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PROSITE; PS00188; BIOTIN; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Delta
565
                                                                                                    505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                      59
                                                                                                                                                                                                                                                     G
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CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = AI
OXALOGGETATE.

COFACTOR: ATP, MAGNESIUM (OR MANGANESE OR COBALT),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HETEROOCTAMER OF FOUR A AND FOUR B SUBUNITS. SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENZYME REGULATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE AFP-DEPENDENT CARBOXYLATION OF THE COVALENTLY ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CROUP TO PYRUVATE IN THE SECOND. THE MAXIMUM ACTIVITY IS AT
  ΜVΙ
                                                                                                                                                                                                                                           VTVNGTAYDVDV-----DVDKSHENPMGTILFGGGTGGAPAPAAGGAGAGKAGEGEIPA
                                                  IKI 121
                                                                                                                      PLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGL 118 : | : | : | : | : | : | : | : | : |
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                                                                                               TMQGMVVKLKVSEGDQVNAGDVVAVVEAMKMENDIQTPHGGVVEKIYTAEGEKVETGDII 564
                                                                                                                                                                                                      VEVDGDEFEVKVVPTGYMTIEEAEPEPVDV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multifunctional enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
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568 1
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63955 MW;
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29.38;
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                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                            Score 141;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                              BIOTIN.
; D328715AB0328DBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRUVATE.
                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no rest
                                                                                                                                                                                                                                                                                                                               DB 1;
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IS AT PH 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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Best Local
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01-OCT-1996 (Rel. :
01-OCT-1996 (Rel. :
15-JUN-2002 (Rel. :
                                                                                                                                                                              01-OCT-1993 (Rel. 27, Created)
01-OCT-1994 (Rel. 30, Last sequence upolicy of the company of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fatty acid biosynthesis; Biotin; Chloroplast.
BINDING ~122 122 BIOTIN (BY SIMILARITY)
SEQUENCE 157 AA; 17519 MW; 5CFF079B2410E777 CRC
                                                                                                                                                                                                                                                                                                                                                                       YEAST
PYC2_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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   SEQUENCE
                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                          P32327;
01-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001249; AcCoA_biotinCC.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR000089; Biotin_lipoy1.
Pfam; PF00364; biotin_lipoy1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U38804; AAC08169.1; -. HSSP; P02905; 1BDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities
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Reith M.E., Munh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Rhodophyta; NCBI_TaxID=2787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porphyra purpurea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biotin carboxyl carrier
                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUNCTION: TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEANKMETEINAPTDGKVEKVLVKE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDIVDCGQALMKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDAVQGGQGLIKI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVSPMVGTFYHSPAPGEKIFVQVGDIVKCNQTVCIIEAMKLMNEIEAEIEGIIIEILVKN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR01071; ACOABIOTINCC.; TIGR00531; BCCP; 1. PS00188; BIOTIN; 1.
FROM
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N.A.,
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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41,
                                                                                                                    Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155
                                                                                          Saccharomycetaceae;
   AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.5%;
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Last sequence update)
Last annotation updat
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CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 138.5;
Pred. No. 0.00
L2; Mismatches
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                                                                                       Saccharomycotina; Sacc
Setaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                    Saccharomycetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 157;
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NP_BIND ACT_SITE

SIMILAR SIMILAR SIMILAR BINDING Pfam; PF00682; HMGL-like; Pfam; PF02436; PYC_OADA; Pfam; PF02785; Biotin_car; Pfam; PF02786; CPSase_L_D

OADA; 1

CPSase_L_D2; 01235; pyruv_ Biotin_carb_C; 1.

35; pyruv_carbox; BIOTIN; 1.

PROSITE;

PROSITE;

.1gase;

Multifunctional PS00866;

Biotin; Gluconeogenesis;

ATP-binding;

CPSASE_

CPSASE_1;

tamily

188 313 1136 331 471

ATP (POTENTIAL).
BY SIMILARITY.
BIOTIN (BY SIMILARITY).
CARBAMOYL PHOSPHATE SYNTHETASES.
WITH OTHER BIOTIN CARRICKTLASES.
WITH OTHER BIOTIN CARRIER PROTEINS AN WITH LIPOAMIDE ACETYLTRANSFERASE.
S -> C (IN REF. 1).

InterPro; IPR000901; CPSase. InterPro; IPR000891; HMGL-like. InterPro; IPR003379; PYC_OADA. Pfam; PF00289; CPSase_L_Chain; 1. Pfam; PF00364; biotin_lipoy1; 1.

SGD;

S0000422; PYC2

InterPro; InterPro;

IPR001882; Biotin_attach.
IPR000089; Biotin_lipoyl.

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the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Scherens B., V
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EMBL; Z36087; CAA85182.1;
EMBL; U35647; AAC49147.1;
PIR; S46094; S46094.
                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288c;
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Stucka R., Dequin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Polymorphism of the yeast pyruvate sifects on protein biotinylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP F
INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE CC
ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER
CARBOXYL GROUP TO PYRUVATE IN THE SECOND.
CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) - AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: BIOTIN AND ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                   AND CARBAMYL PHOSPHATE SYNTHETASES
                                                                                                                                                                                                                                                                                                                                                                                                           INDUCTION: BY GLUCOSE.
SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES,
                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT:
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Vierendeels F
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLUCONEOGENESIS.
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RESULT
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                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                               Read T.D., Brunham R.C., Shen C., Gill S.R., White O., Hickey E.K., Peterson J., Utterbaci Linher K., Weidman J., Khouri H., Craven B., Gwinn M., Nelson W., DeBoy R., Kolonay J., M. Eisen J., Fraser C.M.,
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                                    InterPro;
                                                TIGR;
                                                                                                                                                                                                   NUCLEIC ACIDS RES. 28:1397-1406(2000).

-II- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
-II- CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE
CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE
TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA (BY SImilarity).
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MEDLINE-20150255; Pi
                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biotin carboxyl carrier protein of acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1103
                                                                                                                                                                                                                                                             "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
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16-OCT-2001
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                         InterPro;
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                                               TC0399;
                                                                    AE002306;
                                                                                        an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
IPR001249; AcCoA_DIOLLIUS
IPR001882; Biotin_attach.
IPR000089; Biotin_lipoyl.
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771
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, Utterback T., Berry K
Craven B., Bowman C., E
onay J., McClarty G., S
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CRC64;
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Salzberg
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                                                                                                                                           SEQUENCE OF 1003-1178 FROM N.A.

MEDILINE-87241529; PubMed-3036126;
MOTTIS C.P., Lim F., Wallace J.C.;
MOTTIS C.P., Lim F., Wallace J.C.;

"Yeast pyruvate carboxylase: gene isolation.";
Biochem. Biophys. Res. Commun. 145:390-396(1987).

-1- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE
CARBOXYL GROUP TO PYRUVATE IN THE SECOND.

-1- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phos
                                                                                                                                                                                                                                                                                                                               MEDLINE-97377993; PubMed-9234674;
Feuermann M., de Montigny J., Potier S., Souciet J.-L.;
"The characterization of two new clusters of duplicated ge
suggests a 'Lego' organization of the yeast Saccharomyces
chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1989 (Rel. 11, Created)
01-CCT-1996 (Rel. 34, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Pyruvate carboxylase 1 (EC 6.4.1.1) (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88298805; PubMed=3042770; Lim F., Morris C.P., Occhiodoro F., Wallace J.C.; Sequence and domain structure of yeast pyruvate J. Biol. Chem. 263:11493-11497(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast)
Eukaryota; Fungi; Ascomycota; Saccharomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fatty acid biosynthesis; Biotin; Complete proteome BINDING 127 127 BIOTIN (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                  Yeast 13:861-869(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE-88298805; PubMed-3042770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales;
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                                                                                                  COFACTOR: BIOTIN AND ZINC PATHWAY: GLUCONEOGENESIS.
                                     SUBUNIT: HOMOTETRAMER.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES,
AND CARBAMYL PHOSPHATE SYNTHETASES.
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29.8%;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycotina;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1178
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                                                      LIPOAMIDE TRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carboxylase.";
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    (PCB 1).

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Best Local (
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                                                                                                                   PYC_PICPA STANDARD P78992;
01-NOV-1997 (Rel. 35, C 01-NOV-1997 (Rel. 35, I 15-JUL-1999 (Rel. 38, I Pyruvate carboxylase (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000901; CPSase.
InterPro; IPR000901; MCL-like.
InterPro; IPR003379; PYC_OADA.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00682; HMGL-like; 1.
Pfam; PF00683; PYC_OADA; 1.
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PIR; A29233; QYBYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                    Pichia pastoris (Yeast).
Eukaryota; Fungi; Ascomy
Saccharomycetales; Sacch
                                                                                                                                                                                                                                                                                                                                                                                          1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zinc;
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 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J03889; AAA34843.1; -.
EMBL; Z72584; CAA96765.1; -.
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                                                                                                                                                                                                                                                                                                                                                     116
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                                                                                                                                                                                                                                                                                                                                                     QGLI 119
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PF02786; CPSase_L_D2; 1.
PAMS; TIGG01235; pyruv_carbox;
CTE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                      IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00866; CPSASE_1; PS00867; CPSASE_2;
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                                                    Ascomycota; Saccharon; Saccharonycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.68;
                                                                                                                       Last sequence update)
Last annotation update)
(EC 6.4.1.1) (Pyruvic carboxylase)
                                                                                                                                                                                   Created)
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                                                    Saccharomycotina;
setaceae; Pichia.
                                                                                                                                                                                                                          PRT;
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OTIN (BY SIMILARITY).
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                                                                     Saccharomycetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1178;
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                                                                                                                         (PCB).
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RESULT 17
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Best Local S
Matches 27
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InterPro; IPR003379; PYC_OADA.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF00364; blotin_lipoyl; 1.
Pfam; PF00682; HMGL-11ke; 1.
Pfam; PF02436; PYC_OADA; 1.
Pfam; PF02785; Biotin_carb_C; 1.
                                                                                                                                       16-OCT-2001 (Rel. 40, Cr. 16-OCT-2001 (Rel. 40, La. 15-JUN-2002 (Rel. 41, La. Biotin carboxyl carrier ACCB or CT123.
                                                                                                                                                                                                                                                                                                        BCCP_CHLTR
O84125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
SEQUENCE
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ACT_SITE
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Yeast 14:647-654(1998).
Yeast 14:647-654(1998).
Yeast 14:767-654(1998).

Yeast 14:647-654(1998).

Yeast 14:6
                                                                               Chlamydia trachomatis.
Bacteria; Chlamydiales;
                                                                                                                                                                                                                                                                                                                                                                          CHLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1107
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMs; TIGR01235; pyruv_carbox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y11106; CAA71993.1; -. HSSP; P24182; 1DV1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an
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"Isolation of the Pichia pastoris PYCl gene encoding particles and identification of a suppressor of the
                                                    NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc.
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SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: GLUCONEOGENESIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requires a license agreement (S
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001882; Biotin_attach.
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315
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Last annotation update)
er protein of acetyl-CoA
                                                                                                                                                                                                                                                                       Created)
                                                                                  Chlamydiaceae;
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BY SIMILARITY.
BIOTIN (BY SIMILARITY).
MW; 8B6E858079657914 CRC64;
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Pred. No. 0.00
L1; Mismatches
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                             164
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                                                                                     Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; 1
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e pyc
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RESULT ODDS OF THE PROPERTY OF
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(Rel. 07, Created)

(Rel. 31, Last sequence upda

(Rel. 41, Last annotation up)

(Rel. 41, Last annotation up)

(Rel. 42, Last annotation up)

(Rel. 43, Last annotation up)

(Rel. 41, Last annotation up)

(Rel. 41, Last annotation up)

(Rel. 41, Last annotation up)

(Recomplex (EC 2.3.1.12) (E2).

(Rel. 07, Created)

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Best Local
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Stephens
                                                 STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
  MEDLINE-83234434; PubMed-6345153;
Stephens P.E., Darlison M.G., Lew
                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGREAMS; TIGRO0531; BCCP; PROSITE; PS00188; BIOTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P02905; 3BDO.
PHCI-2DPAGE; 084125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia trachomatis.";
Science 282:754-759(1998).
-!- FUNCTION: THIS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of an
                                                                                                                NCBI_TaxID=562;
                                                                                                                                       Escherichia
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MEDLINE=99000809; PubMed=9784136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fatty acid biosynthesis; Biotin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA (By similarity). PATHWAY: Long-chain fatty acid biosynthesis; first step. SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buropean Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVEKVLVKERDAVQGGQGLIKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE001286; AAC67714.1;
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                                                                   FROM N.A.
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IPR001882; Biotin_attach.
IPR000089; Biotin_lipoyl.
0364; biotin_lipoyl; 1.
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28.2%;
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M.G.,
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2; Mismatches
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                                                                                                                                                          subdivision;
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on update)
  H.M.,
                                                                                                                                                                                                                                                                                                                                                               629
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  Guest J.R.;
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Q., Koonin E.
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                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.";
Biochem. J. 271:139-145(1990).
-!- FUNCTION: The pyruvate deh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Russel G.C., Guest J.R.;
"Overexpression of restructured pyruvate dehydrogenase complexes site-directed mutagenesis of a potential active-site histidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hale G., Perham R.N.;
"Amino acid sequence around lipoic
dehydrogenase multienzyme complex o
dehydrogenase multienzyme j
Biochem. J. 187:905-908(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed properties
in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blattner F.R., Plunkett G. III, Bloch C.A., Perna Riley M., Collado-Vides J., Glasner J.D., Rode C. Riley M., Collado-Vides J., Glasner J.D., Rode C. Ricegor J., Davis N.W., Kirkpatrick H.A., Goeden M.
                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation and characterization domains of the E2p subunit of the Table 10 and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 34-46.
MEDLINE-84256520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence Science 277:1453-1474(1997).
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Nucleotide sequence encoding the dihydrolipoamide acetyltransferase component.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ali S.T.
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MEDLINE-90351365; PubM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-K12 / EMG2;
MEDLINE-97443975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-12
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MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N
STRAIN=K12 / MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lipoamide dehydrogenase (E3).
CATALYTIC ACTIVITY: Acetyl-CoA +
acetyldihydrolipoamide.
L; AE000120; AAC73; A30278; XXECDP.; A16026; A16026.; S45194; S45194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYMMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTORS.
                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EW
                                                                                                                   V01498;
D26562;
                                                                                                                                                                                                             requires a license agreement (
an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                       non-profit institutions as long and this statement is not removed.
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                                                                                                                   CAA24741.1; -. BAA05573.1; -.
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                                                                                             AAC73226.1;
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PubMed=2121129;
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                                                                                                                                                                                                                                                                       Usage
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.K., Mayhew G.F.,
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HSSP; P10802; SWISS-2DPAGE;

1DPC. P06959;

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Q42777; Q42778;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
(EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).
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InterPro; IPR001089; Biotin_lipoyl.
InterPro; IPR004167; Biotin_lipoyl.
InterPro; IPR003016; Lipoyl.
Pfam; PF00198; 2-oxoacid_dh; 1.
Pfam; PF00364; biotin_lipoyl; 3.
Pfam; PF00364; biotin_lipoyl; 3.
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MUTAGEN
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                                         Song
                                                         SEQUENCE FROM N.A., AND SEQUENCE OF N-1
STRAIN-CV. Corsoy 79; TISSUE-Cotyledon;
MEDLINE-94286521; PubMed-8016064;
                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
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  biotin-containing
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                                                                                                                                                                                                                                   Glycine max (Soybean)
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                        'Molecular
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                   J., Wurtele E.S., Nikolau B.J.; ecular cloning and characterization
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m; PD001115; 20xoacid
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terization of the cDNA 3-methylcrotonoyl-CoA
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Pred. No. 0.
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Proc. Natl. Acad
                                                                                                                 BCCP_ANASP
Q06881;
                                                                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rroc. Natl. Acad. Sci. U.S.A. 91:5779-5783(1994).
-!- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3)(-) = ADP
phosphate + 3-methylglutaconyl-CoA.
-!- COFACTOR: Biotin.
                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
ACT_SITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anabaena sp. (strain PCC Bacteria; Cyanobacteria; Cyanobacteria; CBI_TaxID=103690;
                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biotin carboxyl carrier protein of acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U08469; AAA53140.1;
EMBL; U08846; AAA53141.1;
HSSP; P24182; 1BNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entitles requires a license agreement (S or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A., AND SEQUENCE MEDLINE=93352435; PubMed=8102363;
                                                                                                                                         ANASP
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                                                               ACCB OR ALL5057
                                                                                                                                                                                                                                                                                                             SEQUENCE
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n; PF02786; CPSase_L_D2; 1.
SITE; PS00188; BIOTIN; 1.
SITE; PS00866; CPSASE_1; 1.
SITE; PS00867; CPSASE_2; 1.
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ATP (POTENTIAL).
BY SIMILARITY.
BIOTIN (BY SIMILARITY).
R -> K (IN REF. 1; AAA53141).
T -> S (IN REF. 1; AAA53141).
E -> K (IN REF. 1; AAA53141).
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Pred. No. 0.
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MITOCHONDRION.
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01-NOV-1997
16-OCT-2001
15-JUN-2002
                                                                                                                                           ACEF OR ACEB OR PA5016.
                                                                                                                                                                        Dihydrolipoamide acetyltransferase complex (EC 2.3.1.12) (E2).
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                                                                   Bacteria; Proteobacteria;
                                                                                                       Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                       PSEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp. strain protein.";
                                                                                                                                                                                                                                                                                                                                                                                    ODP2_PSEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21595285;
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"Genes for to
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pro; IPRO01249; AcCoA_biotincC.
pro; IPR001282; Biotin_attach.
pro; IPR000089; Biotin_lipoyl.
pr00364; biotin_lipoyl; 1.
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AP003598; BAB76756.1;
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two subunits of acetyl coenzyme A carboxylase of
PCC 7120: biotin carboxylase and biotin carboxyl
                                                                                                                                                                                                                                            (Rel.
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19049 MW;
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30.7%;
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                                                                   subdivision; Pseudomonadaceae
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MEDLINE-20437337; Pubmed-10984043;
Stover C.K. Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.;
Regizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                  SEQUENCE
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Rae J.L., Cutfield J.F., Lamont I.L.;
"Sequences and expression of pyruvate
Pseudomonas aeruginosa.";
J. Bacteriol. 179:3561-3571(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001078; 20xoacid_dh. InterPro; IPR0010089; Biotin_lipoyl. InterPro; IPR004167; E3_binding. InterPro; IPR003016; Lipoyl. Pfam; PF00198; 2-oxoacid_dh; 1. Pfam; PF00364; biotin_lipoyl; 2. Pfam; PF00364; biotin_lipoyl; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acetyldihydrolipoamide.
1- COFACTOR: THE EZ COMPONENT CONTAINS COFACTORS (BY SIMILARITY).
-1- SUBUNIT: FORMS A 24-POLYPEPTIDE STRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3).

-I- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
STRAIN-PAO;
                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD001115; PROSITE; PS00189;
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                                                                                                                                                                                                                                                                                                                                                   BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                  lycolysis;
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APAPAPSESKPAAPAAASVQDIKVPDIGSAGKANVIEVMVKAGDTVEADQSLITLESDKA 160
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P10802; 1E
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520
225
295
                                                                                                                                                                                                                                                                                                                                                                                                  Transferase;
                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC45354.1;
                                                                                                                                                                                                  A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG08401.1;
                                                                                                                                                                                41
159
520
225
301
329
56709
                                                                                                                                                                                                                                                                                                                                                                                                                         20xoacid_dh;
LIPOYL; 2.
                                                                                                                       21.0%;
                                                                                                                                                                                                                                                                                                                                                                                               Acyltransferase; Repeat; Lipoyl;
                                                                                                                                                                                                  ¥
                                                                                             15;
                                                                                                                                                                                             POTENTIAL.

A -> V (IN REF. 1).

GGAGATG -> AVPAPR (IN REF. MQ -> IE (IN REF. 1).

24E15CCC9A590CB4 CRC64;
                                                                                                                       Score 129;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                         LIPOYL
                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY). (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dehydrogenase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ormatics and the EMBL outstation There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWO COVALENTLY - BOUND LIPOYL
                                                                                                                         .005;
                                                                                                                                                 DВ
                                                                                                                                              1;
                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORE
                                                                                                                                              Length
                                                                                             Indels.
                                                                                                                                                 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lagrou M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration -
                                                                                               8
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :
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90

ETEINAPTDGKVEKVLVKERDAVQGGQGLIKI

121

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RESULT 22
PYC_MOUSE
 밁
                                         InterPro; IPR000891; HMGL-like.
InterPro; IPR003879; PYC_OADA.
Pfam; PF00289; CPSase_L_Chain; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00682; HMGL-like; 1.
Pfam; PF02436; PYC_OADA; 1.
Pfam; PF02786; DF0Cin_carbc; 1.
Pfam; PF02786; DF0Sase_LD2; 1.
TIGRFAMS; TIGR01235; PYTUV_carbox; PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, C
01-FEB-1994 (Rel. 28, L
15-JUN-2002 (Rel. 41, L
Pyruvate carboxylase, m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Structure deduced from cDNA sequencing.";

Proc. Natl. Acad. Sci. U.S.A. 90:1766-1770(1993).

Proc. Natl. Acad. Sci. U.S.A. 90:1766-1770(1993).

Proc. Natl. Acad. Sci. U.S.A. 90:1766-1770(1993).

PROCED STATEMENT OF THE FIRST STEP AND THE COVALENTLY

ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE SPECIFIC MANUER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY)

AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.

-I- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis; ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide.
TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                  HSSP; P24182; 1BNC.
SWISS-2DPAGE; Q05920; MOUSE.
                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                   or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Adipocyte;
MEDLINE-93189578; PubMed-8446588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carboxylase) (PCB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q05920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYC_MOUSE
                                                                                                                                                                                                                                                        MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang J., Xia W.L.,
                                                                                                                                                                                                      nterPro; IPR000901;
                                                                                                                                                                                                                AGD; MGI:97520; Pcx.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR00089; Biotin_lipoyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adipose pyruvate carboxylase: amino acid sequence and domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161
                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Mitochondrial matrix.
TISSUE SPECIFICITY: LIVER, KIDNEY, ADIPOSE TISSUE, LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: BIOTIN AND MANGANESE.
PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxaloacetate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND CARBAMYL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: WITH OTHER
                                                                                                                                                                                                                                                                                                   A47255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMEIPSPASGVVESVSIKVGDEVGTGDLILKL 192
                                                                                                                                                                                                                                                                                                                    L09192; AAA39737.1; -.
                                                                                                                                                                                                                                                                                                                                                non-profit institutions as long and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                   A47255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brew K., Ahmad F.;
                                                                                                                                                                                                     CPSase
                                                           pyruv_carbox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOTIN CARBOXYLASES, SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                  There
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ⋧
                                                                                                                                                                                                                                                                                                                                                                                                as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIPOAMIDE TRANSFERASES
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                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
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HSSP; PIR;

C42653; C42653.

P07016; 1C4T. Pro; IPR001078;

InterPro;

IPR001078; 20xoacid_dh.
IPR000089; Biotin_lipoyl.
IPR004167; E3_binding.
IPR003016; Lipoyl.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 28
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ACT_SITE
BINDING
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                           pyruvate dehydrogenase enzyme complex in Acholeplasma laidlawii.";

J. Bacteriol. 174:1388-1396(1992).

-i- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate
                                                                                                                                                                   This
                                                                                                                                                                                                                                                                        dehydrogenase (E1), dihydrolipoam
lipoamide dehydrogenase (E3).
-!- CATALYTIC ACTIVITY: Acetyl-CoA +
                                                                                                                                                                                                                                                                                                                                                          Wallbrandt P., Tegman V., Jonsson B.-H., Wieslander A., "Identification and analysis of the genes coding for the putative pyruvate dehydrogenase enzyme complex in Acholeplasma laidlawii.";
                                                                                            or send an email
                                                                                                                   use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                          between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                            -!- SUBUNIT: FORMS A 24-POLYPEPTIDE
                                                                                                                                                                                                                                                    acetyldihydrolipoamide.
-!- COFACTOR: CONTAINS TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complex (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dihydrolipoamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                     EMBL; M81753; AAA21909.1;
                                                                                                        entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92138635; PubMed=1735725
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Acholeplasmataceae; Acholeplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bactería; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          935489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kcholeplasma laidlawii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-JUN-1994
                                                                                                                                                                                       SIMILARITY: CONTAINS 2 LIPOYL-BINDING DOMAINS.
                                                                                                                                                                                                   SYMMETRY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _ACHLA
                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGQIGAPMPGKVIDIKVAAGDKVAKGQPLCVLSAMKMETVVTSPMEGTIRKVHVTKDMTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amide acetyltransferase 2.3.1.12) (E2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA,
                                                                                           to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1144
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1178
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                                                                                                                                                                                                                                                                                                 dihydrolipoamide acetyltransferase
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BIOTIN CARBOXYLASE (BY SIMILARITY).
CARBOXYLTRANSFERASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BIOTIN (BY SIMILARITY)
W; 14CEA0F9DA8B8127 C
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ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acholeplasmatales;
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                                                                                                                                                                                                                                                                          dihydrolipoamide -
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                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                            There are no rest
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                                                                                                                                                                                                                                                    LIPOYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of.
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                                                                                                                Usage
                                                                                                                                                    and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pyruvate dehydrogenase
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                                                                                                                                          restrictions on
                                                                                                                    and
                                                                                                                                                                                                                                                                            COA
                                                                                                                                                       EMBL
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                                                                                                                                                                 collaboration
                                                                                                                                                      outstation
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RESULT 24
BCCA_MAYCTU
ID ACCA_M
AC P46401
DT 01-NOV
DT 01-NOV
DT 15-JUN
DE CATEOX
GN ACCA1
OC BACTE
OC STRAIN
RX MEDLIN
RA NOTMAI
RA NOTMAI
RA DALE
RT 'Lipid
RT CATEOX
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RA GALL
RT CATEOX
RT SEQUE
RA FLEIS
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RA POLONI
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norman E., de Smet
Dale J.W.;
"Lipid synthesis i
carboxyl carrier p
tuberculosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetyl-/propionyl-coenzyme A carboxylase alpha chain [Includes: Biotin carboxylase (EC 6.3.4.14); Biotin carboxyl carrier protein (BCCP)].
ACCA1 OR BCCA OR RV2501C OR MT2576 OR MTCY07A7.07C.
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycolysis;
BINDING
BINDING
                                                                                                                                      MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavier R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Ouail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
    STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen
Fleischmann R.D., Dodson R., G
Peterson J., DeBoy R., Dodson R., G
Kolonay J.F., Nelson W.C., Umayam I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-50410
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ProDom; PD001115; 20xoacid_dh; 1.
PROSITE; PS00189; LIPOYL; 2.
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PF00364; biotin_lipoyl; 2.
PF02817; e3_binding; 1.
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42; Conserv
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516
544 AA;
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LIPOYL (BY SIMILARITY).
LIPOYL (BY SIMILARITY).
POTENTIAL.
W; 81E92D869CFD5424 CRC64
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                        M.L., Haft
       Ermolaeva
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Hickey E.,
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  Salzberg
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entitles requires a license agreement (See
or send an email to license@isb-sib.ch).
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Submitted (APR-2001)
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SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY: Long-chain fatty acid biosynthesis; first step. SUBUNIT: MULTIMER COMPRISED OF 2 DIFFERENT SUBUNITS, THE ONE (63/64 kDa) HAS BIOTIN CARBOXYLASE AND BIOTIN CARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: Long-chain fatty ac SUBUNIT: MULTIMER COMPRISED
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PF00364; biotin_lipoyl; i
PF02785; Biotin_carb_C; i
PF02786; CPSase_L_D2; 1.
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Pro; IPR000901; CPSase.
PF00289; CPSase_L_chain; 1.
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Z95556; CAB08919.1;
AE007094; AAK46880.1
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CAB08919.1; -.
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ATP + biotin-carboxyl-carrier
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BIOTIN CARBOXYL CARRIER PROTEIN.

ATP (BY SIMILARITY).

BY SIMILARITY.

BIOTIN (BY SIMILARITY).

; FAAOALA46432CABF CRC64;
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Hanemaaijer R., de Kok A., Jolles J., Veeger C.;
"The domain structure of the dihydrolipoyl transacetylase component
of the pyruvate dehydrogenase complex from Azotobacter vinelandil.";
Eur. J. Biochem. 169:245-252(1987).
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                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97234563; PubMed-9119000;
Berg A., Vervoort J., de Kok A.;
"Three-dimensional structure in solution of a
domain of the pyruvate dehydrogenase complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berg A., de Kok A., Vervoort J.;
"Sequential IH and 15N nuclear magnetic resonance assignments and secondary structure of the N-terminal lipoyl domain of the dihydrolipoyl transacetylase component of the pyruvate dehydrogenase complex from Azotobacter vinelandii.";
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Science 255:1544-1550(1992).
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de Kok A., Hol W.G.J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanemaaijer R., Janssen
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Bacteria; Proteobacteria;
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MEDLINE=92196586; PubMed=1549782;
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MEDLINE-89052887; PubMed-3191993;
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                                                                                                                                                                     COFACTORS.
- SUBURIT: FORMS A 24-PO SYMMETRY.
- SIMILARITY: BELONGS TO - SIMILARITY: CONTAINS 3
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FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate to acetyl-coa and CO(2). It contains multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3).

CATALYTIC ACTIVITY: Acetyl-Coa + dihydrolipoamide = Coa + S-acetyldihydrolipoamide.
                                                                                                                                                                                                                                                                                                                        acetyldihydrolipoamide.
COFACTOR: THE E2 COMPONENT CONTAINS THREE COVALENTLY-BOUND LIPOYL
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component of the pyruvate
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Pfam: PF001198; 2-oxoacid_dh; 1.
Pfam: PF00364; biotin_lipoyl; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Biochemical and molecular characterization of the Alcaligenes queurophus pyruvate dehydrogenase complex and identification of a ne type of dihydrollpoamide dehydrogenase.";

I. J. Bacteriol. 176:4394-4408(1994).

I. Bacteriol. 176:4394-4408(1994).

I. PINCTION: The pyruvate dehydrogenase complex catalyzes the over conversion of pyruvate to acetyl-CoA and CO(2). It contains conversion of pyruvate enzymatic components: pyruvate dehydrogenase (E1), dihydrollpoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3).

I. C. I. CAPILYIT ACTIVITY: Acetyl-CoA + dihydrollpoamide = CoA + S-acetyldihydrollpoamide.

I. COPACTORS (BY SIMILARITY).

C. SUBUNIT: FORMS A 24-POLYEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL SYMMETRY.
  Matches
                                                                                                        BINDING
ACT_SITE
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Q59098;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                  BINDING
                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                           ProDom;
                                                                                                                                                                                                                                     Pfam;
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                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-H16 / DSM MEDLINE-94292470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-510;
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                                             Match
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SIMILARITY:
                                                                                                                                                                                                                          rrpro; IPRO01078; 20xoacid_dh.
rrpro; IPRO00089; Biotin_lipoy!
rrpro; IPRO03016; Lipoyl.
rrpro; IPRO03016; Lipoyl.
r; PF00198; 2-oxoacid_dh; 1.
r; PF00364; biotin_lipoyl; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      veen the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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P10802; 1DPC.
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    . Similarity
35; Conser
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                                                                                                                                                                                     00364; biotin_lipoyl; 2.
PD001115; 20xoacid_dh; 1.
PS00189; LIPOYL; 2.
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an email to license@isb-sib.ch).
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Biotin_lipoyl.
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ria; beta subdivision;
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    12;
Score 122; DE
Pred. No. 0.01
L2; Mismatches
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SIMILARITY).
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RESULT 27
PYC_HUMAN
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distinct missense mutations.";
Am. J. Hum. Genet. 62:1312-1319(1998).
-I- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
-INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE
CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TIS
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01-0CT-1989 (Rel. 12, Created)
01-0CT-1996 (Rel. 34, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Pyruvate carboxylase, mitochondrial pr
                                                                                                                                                                        Structural relationship to other biotin-containing carboxylases regulation of mRNA content in differentiating preadipocytes."; J. Biol. Chem. 259:12831-12837(1984).
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver, and Kidney; Walker M.E., Jitrapakdee Submitted (JUL-1995) to t
                                                                                    Seargeant L., Robinson B.H.; "Amerindian pyruvate carboxylase deficiency
                                                                                                                                                                                                                                                                                                propionyl-CoA carboxylase
Arch. Biochem. Biophys. 25
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Mackay N., Rigat B., Douglas C., Chen H.S., Robinson
Mackay Cloning of human kidney pyruvate carboxylase.";
Biochem. Biophys. Res. Commun. 202:1009-1014(1994).
                                                                                                                   Feigenbaum
                                                                                                                                            MEDLINE=98254451; PubMed=958561
                                                                                                                                                           VARIANTS
                                                                                                                                                                                                                                                        SEQUENCE OF 1135-1178 FROM N.A. MEDLINE-85030380; PubMed-6548474;
                                                                                                                                                                                                                                                                                                                          Lamhonwah A.-M., Quan F., Gravel R.A.; "Sequence homology around the biotin-binding site of human
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87212051;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1083-1178 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Kidney
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carboxylase.";
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MEDLINE-95002202; PubMed-7918683;
Wexler I.D., Du Y., Lisgaris M.V.
Yang B.-S., Liu T.-C., Kwon M., P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chordata;
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                                                                                                                                                                                                                             reytag S.O., Collier K.J.;
Molecular cloning of a cDNA for human
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                                                                                                                 M.A., MacKay N., Ling aum A., Clarke J.T.R.,
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PubMed=3555348;
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C., Kwon M., Pai
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254:631-636(1987).
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EMBL/GenBank/DDBJ d
                                                                                                                 Haworth J
                                                                                                                               M., Cole
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                                                                                                                                                          AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V., Mandal S.K., Freytag S.O., Patel M.S., Kerr D.S.; d structure of human pyruvate
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Query Match
Best Local S
Matches 28
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Interpro; IPRO00901; CPSase.
Interpro; IPR000901; CPSase.
Interpro; IPR000891; HMGL-like.
Interpro; IPR003379; PYC_OADA.
Pfam; PF00289; CPSase_L_Chain; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00682; HMGL-like; 1.
Pfam; PF00682; HMGL-like; 1.
Pfam; PF002436; PYC_OADA; 1.
Pfam; PF02436; BYC_OADA; 1.
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TRANSIT 1
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ATP-binding; Mitochondrion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: DEFICIENCY IN PC CAUSES LACTIC ACIDOSIS, MENTAL RETARDATION AND DEATH. OCCURS IN THREE FORMS: TYPE A (MILD); B (SEVERE NEONATAL) AND A VERY MILD LACTICACIDEMIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY) AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE. CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMOTETRAMER.
SUBCELLULAR LOCATION: Mitochondrial matrix.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S01469;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U04641;
$72370;
U30891;
M26122;
K02282;
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  Similarity
28; Conserv
                                                                                                                                                                                                                                                                                                                      Multifunctional
                                                                                                                                                                                                                                                                                                                                 PS00188; BIOTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR0001882; Biotin_attach. IPR000089; Biotin_lipoyl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S01469.
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                                                                                                                                                                                                                                                                                                                                           pyruv_carbox;
             40.6%;
                         19.7%;
                                               129633
                                                                                                                                                                                                                                                                                                          enzyme; Biotin;
ion; Lipid synth
                                             RS -> PT (IN REF. 2).
EL -> DV (IN REF. 2).
P -> R (IN REF. 2).
E -> A (IN REF. 2).
DT -> AP (IN REF. 2).
3 MW; 381F527553A20095 C
  13;
 Score 121; DE
Pred. No. 0.04
l3; Mismatches
                                                                                                                                                       /FTId=VAR_008095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND
                                                                                                               /FTId=VAR_008096.
LA -> WP (IN REF. 2).
A -> S (IN REF. 3).
                                                                                                                                                                          BIOTIN (BY SIMILARITY).
A -> T (IN PC DEFICIENCY
                                                                                                                                                                                                                                                 BIOTIN CARBOXYLASE (BY SIMILARITY)
CARBOXYLTRANSFERASE (BY SIMILARITY
                                                                                                                                                                                                                                     CARBOXYLTRANSFERASE (BY SIMILAR BIOTIN CARBOXYL CARRIER PROTEIN
                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                ATP
                                                                                                                                                                                                                                                                          PYRUVATE CARBOXYLASE
                                                                                                                                                                                                                                                                                   MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                           SIMILARITY)
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                                              381F527553A20095 CRC64;
                                                                                                                                                                                                              (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                           synthesis;
                                                                                                                                                     (IN PC DEFICIENCY TYPE A)
           ; DB 1; Length 1178;
0.043;
                                                                                                                                                                                                                                                                                                                     Manganese; Gluconeogenesis,
                                                                                                                                                                                                                                                                                                         Transit peptide;
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                                                                                                       EMBL; U32314;
EMBL; U36585;
HSSP; P24182;
                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) - ADP + phosphate -

CATALYZES A 2-STEP REACTION, J. 316:631-637(1996).

BIOCHEM. J. 316:631-637(1996).

BIOCHEM. J. 316:631-637(1996).

AUD LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE -

CATALYZES FROM PYRUVATE -

AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.
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P52873;
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                        Pfam;
                                      InterPro;
InterPro;
                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                STRAIN-Wistar; TISSUE-Liver;
MEDLINE-96257760; PubMed-8687410;
Jitrapakdee S., Booker G.W., Cassady A.I., Wallace J.C.;
"Cloning, sequencing and expression of rat liver pyruvate
            Pfam;
                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                 between
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pyruvate carboxylase, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lehn
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COFACTOR: BIOTIN AND MANGANESE (BY SIMILARITY).

COFACTOR: BIOTIN AND MANGANESE (BY SIMILARITY).

PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS.

SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

SUBCELLULAR LOCATION: Mitochondrial matrix.

SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOMINICARBANYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INE=96096548; PubMed=8522203;
D.A., Moran S.M., Macdonald M.J.;
sequence of the rat pyruvate carboxylase-encoding cDNA.";
165:331-332(1995).
                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGDDLILEI 1177
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           PF00289;
PF00364;
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                     IPRO01882; Biotin_attach.; IPRO00088; Biotin_lipoyl.; IPRO09001; CPSase.; IPRO00901; CPSase.; IPRO00891; HMGL-like.; IPRO03379; PYC_OADA.; IPRO03379; PYC_CADA.; IPRO03379; CPSase_L_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Rodentia;
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                                                                                                                    AAA96256.1;
AAC52668.1;
           biotin_lipoyl;
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Best Local :
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BINDING
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-89308706; PubMed-2745462;

Browner M.F., Taroni F., Sztul E., Rosenberg L.E.;

Browner M.F., Taroni F., Sztul E., Rosenberg L.E.;

"Sequence analysis, biogenesis, and mitochondrial import alpha-subunit of rat liver propionyl-CoA carboxylase.";

J. Biol. Chem. 264:12680-12685(1989).
                                                                                                                                                                                                                                                                                                                                                                                     PCCA_RAT P14882;
                                                                                                                                                                                                                                                                                                                               01-APR-1990 (Rel. 14, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Propionyl-COA carboxylase alpha chain, mitochondrial
(EC 6.4.1.3) (PCCase alpha subunit) (Propanoyl-COA:ca
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113
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                               ALPHA SUBUNITS AND SIX BETA SUBUNITS. SUBCELLULAR LOCATION: MITOCHONOCTIA1 IN DISEASE: PROPIONIC ACIDENTA DUE TO REDEFICIENCY OF PCCASE ACTIVITY OFTEN C
                      KETOSIS
                                                                                     PATHWAY: KEY ENZYME IN THE FATTY ACIDS, ISOLEUCINE, TH
                                                                           SUBUNIT: PROBABLY A DODECAMER COMPOSED
   SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGGQGLIKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGDDLILEI 1177
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                      AND
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                      ACIDOSIS
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ATP (BY SIMILARITY.
BY SIMILARITY.
BIOTIN (BY SIM)
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D -> I (IN REF
G -> R (IN REF
G -> R (IN REF
M; 8E5FA19BC1
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                                                                         HE CATABOLIC PATHWAY OF ODD-CHAIN
THREONINE, METHIONINE, AND VALINE.
CAMER COMPOSED OF SIX BIOTIN-CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 119;
Pred. No. 0.
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PYRUVATE CARBOXYLASE.
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> I (IN REF. )
> R (IN REF. )
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                                 TO RECESSIVELY INHERITED FTEN CAUSES LIFE-THREATEN
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(Propanoyl-CoA: carbon diox:
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HCO(3)(-) =
                                 LIFE-THREATENING
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entities
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STRAIN-ATCC 700084 / mc(2)155;
MEDLINE-99328972; PubMed-10400584;
Fernandes N.D., Wu Q.-L., Kong D., Puyang X.,
"A mycobacterial extracytoplasmic sigma facts following heat shock and oxidative stress.";
J. Bacteriol. 181:4266-4274(1999).
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                              the European Bioinformatics Institute.
                                           This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                        use
                                                                                                                                                                     NCBI_TaxID=1772;
                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                      Mycobacterium smegmatis
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                                                                                                                                                                                                                                                                                                                                          C; Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding
                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49799.1; PID:g54583:
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyss1 genome sequence: insights
A;Reference number: A75001
A;Accession: F75135
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C; Comment: Six or 12 chains of biotin carboxyl carrier protein (BCCP) are found onyl coenzyme A to BCCP and (2) from BCCP to pyruvate, forming oxalacetate.
C; Comment: See PIR:A48665 and PIR:S36808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Propionibacterium freudenreichii subsp. shermanii
C;Date: 31-Mar-1980 #sequence_revision 31-Mar-1980 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biotin carboxyl carrier protein [validated] - Propionibacterium freudenreichii subsp. N;Alternate names: methylmalonyl-CoA carboxyltransferase biotin carboxyl carrier prot
                                                                                                                                                                                                                                                                                                                                                                     A;Gene: PAB1771
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-145 <KAW>
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Date: 20-Aug-1999 #sequence_revision
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                                                                                                                           QGGQGLIKIG 70
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Pred. No. 2.1e-27;
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DNA Res. 5, 55-76, 1990
A;Title: Complete sequence and gene organization of the genome A;Reference number: A71000; MUID:98344137; PMID:9679194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: F71133
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C;Species: Pyrococcus horikoshii
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C;Species: Pyrococcus horikoshii
                                                                                                                                                                                                                                 F;537/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                              A; Gene: PH0834
                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                  A; Note: this accession
                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29928.1; PID:g3257245
A;Experimental source: strain OT3
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A; Residues: 1-571 <KAW>
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A; Residues: 1-149 <KAW>
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NA Res. 5, 55-76,
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Res. 5, 55-76,
565 QPLIEL
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36; Conserv
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6, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
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                                                                                                                                                                         Score 180; DB 2;
Pred. No. 1.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NID:g3236132; PIDN:BAA30387.1; PID:g3257704
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Yamazaki,
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Kushida,
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methylmalonyl-CoA dec
C;Species: Archaeoglc
C;Date: 05-Dec-1997 #
C;Accession: H69526
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C;Superf
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C;Date: 08-May-1998 #sequence_revision 08-May-1998
C;Accession: B70432
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Nature 390, 364-370, 1997
pyruvate carboxylase
C; Species: Bacillus c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Klenk, H.P.; Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B70432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pyruvate carboxylase c-terminal domain -
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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                 Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha;572-646/Domain: lipoyl/biotin-binding homology <LPB>;612/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                    GGQGLIKI 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-655 <AQF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              layton, R.A.; Tomb,
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    (EC 6.4.1.1) [imported] cereus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain
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54.7%;
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Pred. No. 6.9e
13; Mismatches
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3; Mismatches
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No. 6.9e-11;
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ches 21;
                       - Bacillus
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                     (fragment)
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hypothetical protein SSO2464 [imported] - C; Species: Sulfolobus solfataricus C; Date: 24-May-2001 #sequence_revision 24-
                                                           RESULT
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24-May-2001

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Sulfolobus solfataricus

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                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Complete genome sequence of the methanogenic A; Reference number: A64300; MUID:96337999; PMID:868808
                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, ; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M. rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, P. Science 273, 1058-1073, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Aug-2000
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A; Experimental source: ATCC 10987
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                                                                                                                                                                                                                                                 A; Map position:
                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                   A;Cross-references: GB:U67563; GB:L77117; NID:g2826379; PIDN:AAB99233.1; PID:g1591862
                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-567 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: F64453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Okstad, O.A.; Hegna, I.; Lindbaeck, T.;
                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; nucleic acid sequence not shown; translation not
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                                                                                                     Similarity
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                                                                                Conservative
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                                                                                12;
                                                                              Score 173; DB 2;
Pred. No. 9.4e-10;
2; Mismatches 2;
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Pred. No. 1.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                   ernanogenic archaeon, Methanococcus jannasc
PMID:8688087
                                                                                                                    Length
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Merrick, J.M.; Glodek,
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pyruvate carboxylase, PYKA [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30 C;Accession: D97227 R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng; Daly, M.J; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: D90418
R;She, Q;; Singh, R.K.; Confalonieri, F; Zivanovic, Y;; A;
Jong, I; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng,
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
C;Accession: C72341
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C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding
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     A; Title:
                                                                                                                                         D97227
                                                                                                                                                         RESULT 11
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A; Residues: 1-134 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: C72341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           propionyl-CoA carboxylase, gamma subunit -C;Species: Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-186 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE001743; GB:AE000512; NID:g4981241; PIDN:AAD35799.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garrett, M.M.; Stewart,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: SSO2464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: AE006641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A99139
A; Accession: D90418
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Best Local
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   Genome
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                                                                                                                                                                                                                                            QGLIKI 69
                                                                                                                                                                                                                                                                            VKAPMAGIVLKVLVKEGQKVNVGDKLLVFEAMKMENELQSEFSGTVKEILVKEGDNIETG 127
                                                                                                                                                                                                            QILMKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K.E.; Clayton, R.A.;
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55.1%;
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 Comparative Analysis
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Cotton, M.D.; Pratt, M.S.; Phillips,
                                                                                                                                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                 14-Sep-2001 #text_change 30-Sep-2001
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les 22;
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Peng, X.; Thi-Ngoc,
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                                                 Zeng, Q.;
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ps, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria
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                                                   Gibson,
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H.P.; Red
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on, D.;
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A; Molecule
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A; Accession: |
A; Status: pre
A; Molecule ty
                         A; Reference number: A82035; A; Accession: G82308
                                                                                         R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                           C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: G82308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:J03885; NID:g149288; PIDN:AAA25120.1; PID:g149289 C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chair C;Keywords: blotin binding; carbon-carbon lyase; carboxy-lyase; sodium pump F;523-596/Domain: lipoyl/biotin-binding homology KLPB>
F;562/Binding site: blotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Schwarz, E.; Oesterhelt, D.; Reinke, H.; Beyreuther, K.; Dimroth, P. J. Biol. Chem. 263, 9640-9645, 1988
A;Title: The sodium ion translocating oxalacetate decarboxylase of Klebsiella A;Reference number: A28088; MUID:88257085; PMID:2454915
A;Accession: A28088
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C; Superfamily:
A; Status: preliminary
                                                                  A; Title: DNA Sequence of
                                                                                                                                                                                                                                           oxaloacetate decarboxylase, alpha chain VC0550 [similarity] - Vibrio cholerae
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                                                                                                                                                                                                                                                                                           RESULT 13
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A; Residues: 1-596 <SCH>
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C; Species: Klebsiella pneumoniae
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A; Residues: 1-1144 < KUR>
A; Cross-references: GB: AE001437;
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Best Local
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35; Conserv
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                                             both chromosomes of the cholera pathogen 35; MUID:20406833; PMID:10952301
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Pred. No. 7.8e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 165; DB 2;
Pred. No. 6.3e-09;
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ATCC824
                                                                                                                                  S.; Qin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 596;
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; Qin, H.; Dragoi,
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R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dods; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.

A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa A; Reference number: A69250; MUID:98049343; PMID:9389475

A; Accession: D69510
                                                                                                                                                                                                                                                                                                                                                                   RESULT
D69510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross references: GB:AE004141; GB:AE003852; NID:g9654976; PIDN:AAF93718.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
                                                                                                                                                                                                                                                                              C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Aug-1999
C;Accession: D69510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: The genome sequence of the food-borne pathogen A; Reference number: A81250; MUID:20150912; PMID:10688204 A; Accession: D81367
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C; Superfamily: 1
A; Molecule type: DNA
A; Residues: 1-142 <KLE>
A; Cross-references: GB: AE000960;
                                                                                                                                                                                                                                                                                                                    oxaloacetate decarboxylase, biotin carboxyl carrier subunit homolog - Archaeoglobus C; Species: Archaeoglobus fulgidus
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A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-599 < PAR>
                                                              A; Status: preliminary; nucleic acid
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33; Conser
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33; Conservative
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50.0%;
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    GB:AE000782;
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Pred. No. 1e-08;
3; Mismatches
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4; Mismatches
                                                                  sequence
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7.9e-09;
19;
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NID: g2689283;
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  PIDN: AAB89171.1;
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                                                                                                                                                                                                                                      K.A.; Dodso
irkness, E.F
    PID: g264844
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C; Genetics:
A; Gene: Atu:
A; Map positi
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C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding F;66-139/Domain: lipoyl/biotin-binding homology <LPB>
                                     homology
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Query Match
                                                       Local Similarity
                     1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV
Conservative
                                                     47.18; 50.88;
                                           13;
                                        Score 161; DB 2; ...
Pred. No. 3.6e-09;
"'amatches 18;
                                           Indels
                                           0
                      60
                                           0
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63

biotin carboxylase protein A2 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Decies: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 C;Accession: H98247 C58, Cer

R;Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger, Science 294, 2323-2328, 2001 χ. (). Miller, N.; E Doughty, D.; and Biotechnology Blanchard, M.; ; Scott, C.; La Lappas, Agent Agrobacterium Qurollo, B.; Goldm Markelz,

A;Title: Genome Sequence of the Plant Pathogen A;Reference number: A97359; PMID:11743194 A;Accession: H98247 A;Status: preliminary

A; Molecule type: DNA A; Residues: 1-576 < KUR> A; Cross-references:

Genetics: GB:AE007870; PIDN:AAK89506.1; PID:g15159380; GSPDB:GN00170

Query Match Local Similarity es 35; Conserv 46.6%; 13; Score 159.5; Pred. No. 2.2e 13; Mismatches 2.2e-08; ches 20; DB 2; 1. Gaps ۲,

biotin carboxylase homology;

EGEMTAPVSGTLQSFKVKDGETVSEGDLLAVMEAMKMETQIVATRAGKV-RLIVKEGDYL EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV

61 QGGQGLIKI 69

biotin carboxylase [imported] - Agrobacterium tumefaciens (strain C58, Dupo C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002

C; Date: 1.1.
C; Accession: AC3038
C; Accession: AC3038
R; Wood, D. W.; Setubal, J.C.; Kaul, R.; Monks, R; Wood, D. W.; Setubal, J.C.; Guenthner, erage, G.; Gillet, W.; Grant, C.; Guenthner, Erage, G.; Gillet, W.; Grant, C.; Guenthner, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001 P.; Jung, M.; Krespan, W.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo thner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl Perry, M.; Gordon-Kam

Natural Genetic Engineer ; PMID:11743193 Agrobacterium tumefaciens C58

A;Title: The Genome of the I A;Reference number: AB2577; A;Accession: AC3038

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-576 < KUR>

A;Cross-references: GB:AE008689; PIDN:AAL44721.1; PID:g17742353; GSPDB:GN00187 A;Experimental source: strain C58 (Dupont)

Atu3913

linear

C; Superfamily:

propionyl-CoA carboxylase alpha chain;

lipoy

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A;Gene: PA5435
C;Superfamilv:
                                                                                                                                                                                                                  adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V.
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A;Title: Mechanisms of Evolution in Rickettsia conorii and A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: G97819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: G97819
R; Ogata, H.; Audic,
Science 293, 2093-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source:
                                                                                             A;Cross-references: GB:AE004956; GB:AE004091; A;Experimental source: strain PAO1
                                                                                                                       A; Residues: 1-607 <STO>
                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                             A; Reference number: A82950; A; Accession: F82966
                                                                                                                                                                                                      .; Lory, S.; Olson, Nature 406, 959-964,
                                                                                                                                                                                                                                             R;Stover, C.
                                                                                                                                                                                                                                                            C; Accession: F82966
                                                                                                                                                                                                                                                                                  probable transcarboxylase subunit PA5435 [imported] -
C;Species: Pseudomonas aeruginosa
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C; Superfamily:
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A; Residues: 1-665 < KUR>
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Best Local S
Matches 33
                                                                                Genetics:
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Best Local
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                                                                                                                                                                                                                                           .K.; Pham, X.Q.;
             Similarity
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                                                      Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           propionyl-CoA carboxylase alpha chain; biotin carboxylase homology;
                                                                                                                                                                                                                                                                                                                                                                   663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                       2000
                                                                                                                                                                           sequence of Pseudomonas aeruginosa 50; MUID:20437337; PMID:10984043
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 46.2%; Score 158; D)
48.5%; Pred. No. 3.20
Live 12; Mismatches
                                                    pneumoniae oxaloacetate decarboxylase alpha
                                                                                                                                                                                                                               Erwin,
L.L.; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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Pred. No. 2.2
                                                                                                                                                                                                                               Coulter, S.N.; Fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 159; DB 2;
Pred. No. 2.8e-08;
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Mismatches
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             3.2e-08;
                                                                                                         NID:g9951760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                               hi, S.D.; Warrener,
Folger, K.R.; Kas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                      #text_change 31-Dec-2000
                         Length 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 665,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsia prowazekii.
                                                                                                         PIDN: AAG08820.1;
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                                                    chain;
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Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
0;
                                                    lipoyl/bio
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                                                                                                                                                                                                                             M.J.; Br
K.; Lim,
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A; Residues: 1-1146 <GLA>
A; Cross-references: GB:AL592022; PIDN:CAC96291.1;
A; Experimental source: strain Clip11262
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                                                                                                  Qy
                                                                                                                                                                                                          A; Gene: pycA
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                  ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Ve A;Title: Comparative genomics of Listeria species A;Reference number: AB1077; MUID:21537279; PMID:11 A;Accession: AC1565
                                                                    片
                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                            D.; Jones, L.M.; Karst, Science 294, 849-852, 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Glaser, P.; Frangeul, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: AC1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pyruvate carboxylase homolog pycA [imported] - Listeria innocua (strain Clip11262)
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                                                                                                                                       Query Match
Best Local S
Matches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .; Dominguez-Bernal,
1138 DLLIEV 1143
                                                               1078 VGATMTGSVIQVVVKKGDSVKKGDPLLITEAMKMETTIQAPFDGEVSSIYVSDGDTIESG 1137
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                                                                                     4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
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                                                                                                                                                          Similarity
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                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duchaud, E.; Durand,
                                                                                                                                    45.9%; Score 157; DB 2;
43.9%; Pred. No. 7.9e-08
tive 17; Mismatches 20
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                                                                                                                                                                                                                                                                               PID:g16413519;
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Dussurget, O.;
                                                                                                                                                                       Length 1146;
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J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F.; Berche, P.; Entian, K.D.;
                                                                                                                                                                                                                                                                                 GSPDB:GN00178
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Waitournam, A.;
Voss, H.; Wehla
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Fsihi,
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pyruvate carboxylase homolog pycA [imported] - Listeria monocytogenes (strain C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 EGD-e)

C; Accession: AH1208

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.I Science 294, Jones, L.M.; Karst, 849-852, Kunst, F.; Kurapkat, G.; Madueno, N.; Tierrez, A.; Vazquez-Boland, J . P E Waitournam, Voss, H.; W he, P.; K.D.; F ; Bloec Fsihi, 2

A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F., ok, C.; Schlueter, T.; Simoes, N.; Tierre, A;Title: Comparative genomics of Listeria

Wehla

A;Status: preliminary

A; Ncdrus. F.--... A; Molecule type: DNA A; Residues: 1-1146 <GLA> A; Cross-references: GB:NC_003210; PIDN:CAC99150.1; A; Cross-references: Strain EGD-e PID:g16410474; GSPDB:GN00177

pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bindi

Best Local Matches : . Similarity 29; Conserv 45.98; 17; Pred. No. 7.9 '; Mismatches 7; DB 2; . 7.9e-08; cches 20; Gaps

Score 157;

Length 1146

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62

GGQGLIKI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 18-Aug-2000
C;Accession: F70439
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C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: A83978
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A83978
pyruvate carboxylase pycA [imported] - Bacillus halodurans (strain C-125)
C;Species: bacillus halodurans
                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE000747; NID:g2983944; PIDN:AAC07497.1; A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                A; Residues: 1-620 <AQF>
                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oxaloacetate decarboxylase alpha chain - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06344.1; GSPDB:GN0(
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: A83978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno,
                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                       Query Match
Best Local
                                                                                                                                                             Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha;540-613/Domain: lipoyl/biotin-binding homology <LPB>;579/Binding site: biotin (Lys) (covalent) #status predicted
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      545
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GDVTSPITGKVVNIKVNVGDEVKEGDVLLVVEAMKMENEIHSPVDGIVEEIFVRVGETVN 604
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                                      GEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQ 61
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                                                                                                       Similarity
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larity 45.6%;
Conservative 1
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                                                                               Score 153; DB 2
Pred. No. 1e-07;
14; Mismatches
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Pred. No. 7.9e-08;
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                                                                                                                        DB 2;
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                                           Matches
                                                            Query Match
Best Local
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R;Burton, N.P.; Williams, T.D.; Norris, P.R. submitted to the EMBL Data Library, January A;Description: Biotin carboxylase, carboxyl
                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-167 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z22744
A; Accession: T44291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biotin carboxyl carrier protein [imported] - Sulfolobus metallicus
C; Species: Sulfolobus metallicus
                                                                                                                                                                                                                                                                                  A; Kestudes: 1 10, 2000.
A; Cross-references: EMBL: AF042099;
Cross-references: EMBL: AF042099;
                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated
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                                                                                                                                                             Matches
                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession:
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158 KKGDLLV
                                    61 QGGQGLI 67
                                                                            98 EGEVLSPLOGRVVAIRVKEGDAVTKGOPLLSVEAMKSETIISAPIAGVIEKIAVKPGOGV 157
                                                                                                                                                                              Local Similarity
                                                                                                                1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
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                                                                                                                                                         Conservative
                                                                                                                                                                              44.48;
                                                                                                                                                                            Score 152; DB 2;
Pred. No. 3.4e-08;
                                                                                                                                                                                                                                                                                                                                                                   from
                                                                                                                                                                                                                                                                                                                                                                                                                            carboxyl carrier
                                                                                                                                                                                                                                                                                                     PIDN: AAB97085.1
                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                            protein and putative carboxyl
                                                                                                                                                                                                 Length 167
                                                                                                                                                             Indels
                                                                                                                                                         0
                                                                                                                                                       Gaps
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A;Description: catalyzes the formation of 3-methylglutaconyl-CoA (3-methyl-2-pentened C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; l1 C;Keywords: biotin binding; ligase F;362-435/Domain: lipoyl/biotin-binding homology <LPB> F;401/Binding site: biotin (Lys) (covalent) #status predicted A;Molecule type: mRNA A;Residues: 367-369,'V',371-373,'V',375-376,'E',378-436 <HOF> A;Cross-references: EMBL:Y00144; NID:g19174; PIDN:CAA68339.1; Nucleic Acids Res. 15, 3928, 1987
A; Title: A tomato cDNA encoding a biotin-binding protein A; Reference number: A29271; MUID:87231088; PMID:3588314 A;Cross-references: GB:U07745; NID:g497180; PIDN:AAA19157.1; A;Experimental source: var. Rutgers A; Molecule type: mRNA A; Residues: 1-436 <WAN> A; Reference number: A53568; A; Accession: A53568 R; Wang, X.; Wurtele, E.S.; Keller, G.; McKean, A.L.; J. Biol. Chem. 269, 11760-11769, 1994
A; Title: Molecular cloning of cDNAs and genes coding methylcrotonoyl-CoA carboxylase (EC 6.4.1.4) biotin-binding chain - tomato (fragment) C;Species: Lycopersicon esculentum (tomato) C;Date: 19-Mar-1997 #sequence_revision 30-May-1997 #text_change 11-Jan-2002 C; Function: A; Accession: A29271 R; Hoffman, N.E.; Pichersky, E.; ;Accession: A53568; A29271 or cunas and genes coding for MUID:94216274; PMID:8163472 Cashmore, A.R. A.L.; Nikolau, beta-methylcrotonyl-CoA carb PID:g497181 B.J PID:g19175

N

Similarity 32; Conserv

44.48;

Score 152; DB Pred. No. 9.1e L1; Mismatches

DB 2; .1e-08;

Length 436

Indels

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Gaps

0

GEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQ 61

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Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: E83791
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                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein BH1133 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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A; Residues: 1-70 <STO>
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A; Residues: 1-591 < WOE>
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J. Biol. C
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Best Local S
Matches 31
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                                                 GQGLIKI 69
                                                                                              EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQG 62
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f the sodium ion pump oxaloacetate decarboxylase
A44465; MUID:93054591; PMID:1331067
                                                                                                                                                                                                                                                    GB:AP001511; GB:BA000004; ce: strain C-125
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Pred. No. 2.
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Pred. No. 1.3e-07;
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                                                                                                                                                NID:g10173727; PIDN:BAB04852.1;
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propionyl-COA carboxylase alpha chain precursor (pccA) RP618 - Rickettsia prowazekii C.Species: Rickettsia prowazekii C.Species: Rickettsia prowazekii C.Species: Z1-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 C.Accession: C71667 R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,,...s-references: GB:AJ235272; GB:AJ235269; NID:g3861033; A;Experimental source: strain Madrid E C;Genetics:
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                                                                                                                                                                                                            C; Superfamily: Klebsiella pneumoniae oxaloacetate C; Keywords: carbon-carbon lyase; carboxy-lyase
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C:Superfamily: propionyl-CoA carboxylase alpha chain; biotin F;592-665/Domain: lipoyl/biotin-binding homology <LPB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The genome sequence of Rickettsia A;Reference number: A71630; MUID:99039499; A;Accession: C71667
                                                                                                                                                                                                                                                                                                                                                                                                  A; Authors: Parry, C.; Quail, M.; Rutherford, K.; A; Title: Complete genome sequence of a multiple carreference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: this species has also been call C; Date: 09-Nov-2001 #sequence_revision
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A; Residues: 1-591 <PAR>
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                                                                                                                                                                                                                                                       A; Gene: oadA
                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AL513382;
                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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A; Residues: 1-665 < AND>
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                                                                                                                          Score 148; DB Pred. No. 3.2e. 0; Mismatches
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Pred. No. 2.3e-07;
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PMID:9823893
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drug resistant
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Salmonella enterica
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C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biot
C;Keywords: carbon-carbon lyase; carboxy-lyase
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Search completed: May 1, 2003, 07:50:28 Job time: 11.5729 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AE0909
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Nature 413, 848-852, 2001
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A;Molecule type: DNA
A;Residues:'1-591 <PAR>
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Result No.

PCCA_HUMAN
BCCP_CHLPN
ODO2_MYCTU
BTB7_MYCLE

2 rattus norv 5 homo sapien 1 chlamydia p 1 mycobacteri 9 mycobacteri

RESULT

ALIGNMENTS

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BCCP_PROFF

BCCP_PROFF

BCCP_PROFF

PO2904

PO2904

DT 21-JUI

DT 15-JUN

DE Biotin

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutagenesis.";
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Ericsson L.H., Walsh K.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biotin carboxyl carrier protein of methylmalonyl-CoA carboxyltransferase (Transcarboxylase, 1.3S subunit).
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J. Biol. Chem. 254:11615-11622(1979)
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Proc: Nath: Acad: SC1.-U.S.A. 82:5617-5621(1985)
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Bacteria; Actinobacteria; Actinobacteria (class);
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15-JUN-2002 (Rel.
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            Conservative
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                                                                                       AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267:18407-18412(1992)
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                        Score 342; DB 1; Pred. No. 1.1e-27;
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MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Scott J.L., Geoghagen N.S.M., Weidman J.D., Sudow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii";
                                                                                                                                                                                                                                                                                                                                              "A stable archaeal pyruvate carboxylase from the hyperthermophile methanococcus jannaschii.";
Arch. Microbiol. 174:406-414(2000).
-I- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL GROUP TO PYRUVATE IN THE SECOND.
-I- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanocaldococcaceae; Me
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30-MAY-2000 (Rel.
15-JUN-2002 (Rel.
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         European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial itles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                       SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                     PATHWAY: GLUCONEOGENESIS.
SUBUNIT: HETEROOCTAMER OF FOUR A AND FOUR B SUBUNITS
MASS SPECTROMETRY: MW-64160; METHOD-MALDI.
                                                                                                                                                                                                                                                                                                            OXALOACETATE.
COFACTOR: ATP, MAGNESIUM (OR MANGANESE OR
                                                                                                                                                                                       MISCELLANEOUS: ITS OPTIMUM PH IS
                                                                                                                                                                                                                                                                                   ENZYME REGULATION:
                                                                                                                                                                                                                                                     KETOGLUTARATE
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                                                                                                    SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                         IS 80-90 DEGREES CELSIUS
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Methanocaldococcus.
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AND FUNCTION.
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Best Local
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                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                      HSSP;
                                                                                                                                                        This
                                                                                                                                                                                                                 pneumoniae. Sequence of the biotin-containing alpha-subunit relationship to other biotin-containing enzymes.";
J. Biol. Chem. 263:9640-9645(1988).
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01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                     P13187;
01-JAN-1990
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                                                                                                                                                                                                                                                Schwarz E., Oesterhelt D., Reinke H., Beyreuther K., Dimroth P.; The sodium ion translocating oxalacetate decarboxylase of Klebsiella
                                                                                                                                                                                                                                                                    MEDLINE=88257085; PubMed=2454915;
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PF00682; HMGL-like; 1.
PF02436; PYC_OADA; 1.
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IPR000089; Biotin_lipoyl.
IPR000891; HMGL-like.
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IPR000891; HMGL-like.
IPR003379; PYC_OADA.
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Cyaloacetate decarboxylase alpha chain (EC 4.1.1.3)
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STRAIN-LT2 / SGSC1412 / ATCC 700720;
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J. Biol. Chem. 267:227
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K. Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

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A Kucha K., Matsuda H.A., Ashburner M., Baldarelli R., Barsh G.,

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A Burownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

A Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

A Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.
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StyGene; SG7777; oadA2.
StyGene; SG7777; oadA2.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR00089; Biotin_lipoyl.
InterPro; IPR000891; HMGL-like.
InterPro; IPR00379; PYC_OADA.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00582; HMGL-like; 1.
Pfam; PF00682; HMGL-like; 1.
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Q99MRB; Q9DBR2;
15-JUN-2002 (Rel. 41, C
15-JUN-2002 (Rel. 41, I
15-JUN-2002 (Rel. 41, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baumgartner M.R., Almashanu S., Suormala T., Obie C., Cole R.N Packman S., Baumgartner E.R., Valle D.;
"The molecular basis of human 3-methylcrotonyl-CoA carboxylase deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INIT_MET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
(EC 5.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subunit) (3-methylcrotonyl-CoA:carbon
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32; Conserv
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590 AA;
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O BY SIMILARITY.

6 BIOTIN (BY SIMILARITY).

63075 MW; 4EA421F9324AFD7B CRC64;
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Sciurognathi; Muridae;
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; Murinae; Mus
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        O N.,
, Storch K.-F.,
<sup>134</sup>lming L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         590;
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Best Local :
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InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR0000901; CPSase.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00785; Biotin_carb_C; 1.
Pfam; PF02786; CPSase_L_D2; 1.
PROSITE; PS001867; CPSASE_2; 1.
                                                                                                      ACT_SITE
BINDING
DOMAIN
                                                                                 CONFLICT
                                                                                                                               ACT_SITE
                                                                                                                                                                                                                                                                                                                EMBL; AF310338; AAG50244.1;
EMBL; AK007782; BAB25253.1;
EMBL; BC021382; AAH21382.1;
HSSP; P24182; 1DV1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              This
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                                                                                                                                                                                                                                                                                                       MGD; MGI:1919289; Mcccl.
                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                      SEQUENCE
                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                     between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wynshaw-Boris A., Yoshida K.,
Hayashizaki Y.;
                                                                                                                                                                                        Mitochondrion;
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                                                                                                                                                                             RANSIT
 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKE 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitted (JAN-2002) to the EMBL/GenBan CATALYTIC ACTIVITY: ATP + 3-methylo phosphate + 3-methylglutaconyl-CoA. CCFACTOR: Biotin.
                                                                                                                                                                                                                                                                                                                                                                                                         swiss-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Leucine catabolism.
SUBUNIT: Probably a dodecamer composed of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Mitochondrial matrix (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha subunits and six beta subunits.
                                   Similarity
                                                                  324
507
717
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335
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709
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335
677
714
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50.0%;
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+ 3-methylcrotonyl-CoA + HCO(3)(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       full-length
                                   Score 148;
Pred. No. 1
                                                                               ≯ ₹
                                                                                                      ATP (POTENTIAL).
BY SIMILARITY.
BIOTIN (BY SIMILARITY).
POLY-GLU.
                                                                                                                                                  CHAIN
                                                                                                                                                               METHYLCROTONYL-COA
                                                                                                                                                                            ; ATP-binding; Transit peptide
MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                   -> K (IN REF. 3).
-> P (IN REF. 1).
F653FE7AC1E5AA90 CRC64;
                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse cDNA
                                   DB 1;
.6e-07;
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                                              Length 717
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                        Indels
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밁 BCCP_STRMU P29337; 01-DEC-1992 01-DEC-1992 01-NOV-1997 Biotin carboxyl carrier protein (BCCP). Streptococcus mutans. Streptococcus Bacteria; Firmicutes; STRMU 642 σ QGGTIAPMTGTIEKVFVKAGDRVKAGDSLMVMIAMKMEHTIKAPKDGRIKKVFFSE (Rel. STANDARD; 24, 35, Last sequence update) Lactobacillales; Streptococcaceae; Created) PRT; 130 update) 697

NCBI_TaxID=1309

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RESULT
BCCP_LY
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Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                        MEDLINE-87231088; PubMed-3588314;
Hoffman N.E., Pichersky E., Cashmore A.R.;
"A tomato cDNA encoding a biotin-binding protein.";
Nucleic Acids Res. 15:3928-3928(1987).
-1- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
-1-CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE
CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE
TRANSFERS THE CARROXYL GROUP TO FORM MALONYL-COA.
use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                      This
                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryop
Spermatophyta; Magnoliophyta; eudicotyledons; c
Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fatty acid biosynthesis; Biotin. BINDING 96 96 BIOSEQUENCE 130 AA; 13601 MW; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M80523; AAA03702.1; -. HSSP; P02905; 1A6X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BioTechniques 14:209-212(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-UT-041 / Se
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                           Biotin carboxyl carrier protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCCP_LYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Blotin-containing protein as a cause of false positive clones yene probing with streptavidin/biotin.";

31oTechniques 14.706.717.777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEDLINE=93159778; PubMed=8431283;
                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                ycopersicon esculentum (Tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                        European Bioinformatics Institute.
                                                                                                                 PATHWAY: Long-chain fatty acid biosynthesis; first SUBCELLULAR LOCATION: Chloroplast.
                                                                      SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNLITI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the El
European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGLIKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001882; Biotin_attach.
IPR000089; Biotin_lipoyl.
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13601 MW;
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47.08;
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acetyl-CoA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
                                                                                                                                                                                                                                                                                                   Embryophyta; Tracheo edons; core eudicots; anaceae; Solanum.
                                        There are no rest
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.8e-08;
les 27;
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             . Usage by and for commercial http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                               Tracheophyta;
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                                                                                                                                                                                                                                                                                                Obata K., Fukuda T., Morishita R., Abe S., Asakawa S., Yamaguchi S., Yoshino M., Ihara K., Murayama K., Shigemoto K., Shimizu N., Kondo I "Human biotin-containing subunit of 3-methylcrotonyl-coa carboxylase gene (MCCA): cDNA sequence, genomic organization, localization to chromosomal band 3q27, and expression.";

Genomics 72:145-152(2001).
SEQUENCE
HIS-532.
                                                                                           Roscher A.A.; Cloning of the human MCCA and MCCB genes and the molecular cause of 3-methylcrotonyl-CoA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 096RQ3; Q9H959; Q9NS97;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallardo M.E., Desviat L.I
Perez-Cerda C., Perez B.,
Morton D.H., Gibson K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Last annotation update)
Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
(EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 1) (MCCase alpha
subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001882; Biotin_attach.
InterPro; IPR000089; Biotin_lipoy1.
Pfam: PF00364; biotin_lipoy1; 1.
PROSITE; PS00188; BIOTIN; 1.
                                                              deficiency.";
Hum. Mol. Genet.
                                                                                                                                                                              Holzinger A., Roeschinger W., La
Kattenfeld T., Thuy L.P., Nyhan
                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND VARIANT MEDLINE-21299419; Pubmed-11406611
                                                                                                                                                                                                                                                                                 Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21295033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Am. J. Hum. Genet.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ugarte M., Penalva M.A.;
"The molecular basis of 3-methylcrotonylglycinuria,
leucine catabolism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11170888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MCCA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fatty acid biosynthesis; Biotin; Chloroplast NON_TER 1 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCCC1 OR MCCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                œ
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A29271; A29271.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Human).
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                     N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                              10:1299-1306(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=11401427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35
7416 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68:334-346(2001).
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND VARIANT HIS-464.
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48.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L.R.,
                   VARIANTS MCGI VAL-289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS MCGI ARG-325
                                                                                                                                                                                W., Lagler F., Mayerhofer P.U., Lichtner Nyhan W.L., Koch H.G., Muntau A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R., Rodriguez J.M., Rodriguez-Pombo P., Le T.P., Ribes A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 143;
Pred. No. 4.
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D75D018C0BD016BC CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                    MCGI
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                                                                                                                                                                                                                                                      PHE-535
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ies 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Esparza-Gordillo, Criado O., Sanz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rodriguez
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                                                                                                                                  mutations
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                   SER-385; PRO-437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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InterPro; IPROUDUU; Crousci, 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF02786; CPSase_L_D2; 1.
DBOSTTE: PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
ACT_SITE
BINDING
               VARIANT
                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
                                                                     VARIANT
                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isogai T., Ota T., Hayashi K., Sugiyama T.,
Nishikawa T., Nagai K., Sugano S., Aotsuka (
Matsunawa H., Ishii S., Kawai Y., Saito K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baumgartner M.R., Almashanu S
Packman S., Baumgartner E.R.,
"The molecular basis of human
                                                                                     DOMAIN
                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakamura Y., Nagahari K., Masuho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       InterPro; IPR000089;
                                                                                                                                                                                                                                                                                                                                                                Genew;
                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                                                                                                                                                              isease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Mitochondrial matrix DISEASE: Defects in MCCC1 are the cause of methylcrotonylglychnuria type I (MCGI, CGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atrophy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recessive disease that is characterized atrophy, probably of spinal origin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Probably a dodecamer composed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest
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AF297332;
AF310339;
AK023051;
BC004214;
BC004187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF310972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lpha subunits and six beta subunits.
                                                                                                                                                                                                                                                                                                                                                              HGNC:6936;
                                                                                                                                                                                               mutation;
                                                                                                                                                                                                                         PS00867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and this statement requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM
                                                                                                                                                                                                                                                                                                      IPR001882; Biotin_attach.
IPR000089; Biotin_lipoyl.
IPR0000901; CPSase.
                                                                                                                                                                                                                                                                                                                                    IPR001882;
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               385
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                                                                                                                                                                                                            Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107:495-504(2001).
                                                                                                                                                                                              Polymorphism
                                                                                                                                                                                                                        CPSASE_2;
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339
681
541
718
289
              385
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+ 3-methylcrotonyl-CoA + HCO(3)(-) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ai Y., Saito K., Yamamoto J., asuho Y., Sasaki N.; project."; Project.";
/FTId=VAR_012786.
R -> S (IN MCGI,
/FTId=VAR_012787.
                                                                                                                          ATP
                                      /FTId-VAR_012785
                                                                                                POLY-SER.
                                                                                                             BIOTIN (BY SIMILARITY)
                                                                                                                                                                 MITOCHONDRION (POT)
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                                                                                                                                                                                                          ATP-binding; Transit peptide;
                                                                                                                          SIMILARITY
                                                                                                                                      (POTENTIAL).
                                                                  V (IN MCGI,
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by
                                                                                                                                                                              (POTENTIAL)
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S., Yoshikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of six
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            SEVERE FORM).
                                                                   MILD
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                                                                  FORM)
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wa Y.,
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                                                                                      RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Linzo C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RSquence and analysis of chromosome 1 of the plant Arabidopsis
T thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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SEQUENCE
STRAIN-cv. Columbia;
Shinozaki K., Davis
"RIKEN Arabidopsis f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last annotation update)
Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
(EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha
subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).
MCCA OR ATIG03090 OR F1003_8 OR F1003.9.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                          MEDLINE-21016719; PubMed-11130712; Theologis A., Ecker J.R., Palm C.J
                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning of the biotinylated coenzyme A carboxylase of Arabidopsis to Plant Physiol. 107:1013-1014(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE .....
STRAINECV. Columbia;
MEDLINE-95232183; PubMed-7716229;
MEDLINE-95232183; Prophed-7716229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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Q42523; Q9
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                                                                        Nature
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Wurtele E.S., Nikolau B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3702;
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15-JUN-2002 (Rel. 41,
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                                Columbia;
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725
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P -> H
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Pred. No. 5
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D -> H / TIV
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S -> F (IN MCGI,
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 J.R., Theologis A.; cDNA clones (RAFLs)
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.F., Chin C.W.,
Creasy T.H., Dewar K.
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CRC64;
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Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-methylcrotonyl-CoA carboxylase.
J. Biol. Chem. 275:5582-5590(2000)
-i- CATALYTIC ACTIVITY: ATP + 3-me
                                                                                                                                                                                                                                                                                                                            PROSITE; PS0018B; BIOTIN; PROSITE; PS00866; CPSASE_PROSITE; PS00867; CPSASE_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSP consortium (Salk/Stanford/PGEC).";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- CAUTION: Ref.2 sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-cv. Landsberg erecta, and cv. Columbia; MEDLINE-20148760; PubMed-10681539;
                                                                                                                                                                                                                                                                                                    TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                    665
                         62
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COFACTOR: Biotin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Probably a heterodimer composed of biotin-containing alpha subunits and beta subunits (By similarity).
SUBCELLULAR LOCATION: Mitochondrial matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: Temporal and spatial accumulation of the beta subunits during development at approximately equal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: In roots, cotyledons, ovaries, siliques and embryos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: Leucine catabolism.
SUBUNIT: Probably a heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene model prediction.
                                                                             GEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQ 61
DGSALFRI 732
                           GGQGLIKI 69
                                                                                                                                                                                                                                                                                                                                                                   PF02785; Biotin_carb_C; 1.
PF00364; biotin_lipoyl; 1.
PF00289; CPSase_L_chain; 2.
PF02786; CPSase_L_D2; 2.
                                                  GTIVAPMAGLVVKVLVENEAKVDQGQPILVLEAMKMEHVVKAPSSGSIQDLKVKAGQQVS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC006550; AAD25800.1; ALT_SEQ AY070723; AAL50065.1; -. P24182; IBNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U12536; AAA67356.1;
                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                            PS00866; CPSASE_1; 1. PS00867; CPSASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001882; Biotin_attach.
IPR000089; Biotin_lipoyl.
IPR000901; CPSase.
                                                                                                                                                                                                                                                                                 Ligase;
1 25
26 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTIVITY: ATP + 3-methylcrotonyl-CoA +
3-methylglutaconyl-CoA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Song J.,
                                                                                                                   41.8%;
45.6%;
                                                                                                                                                              80451
                                                                                                                                                                                                                                                                                                                Biotin;
                                                                                                                                                              MW.
                                                                                                        10;
                                                                                                                                                                          ATP (POTENTIAL)
BY SIMILARITY.
BY OTIN (BY SIMILARITY).
V -> D (IN REF. 1).
A -> AK (IN REF. 1).
MISSING (IN REF. 1).
W -> L (IN REF. 1).
                                                                                                       Score 143; DB
Pred. No. 5.3e
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              differs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Che P., Achenbach S., Nikolau B.J.,
                                                                                                                                                                                                                                                                       METHYLCROTONYL-COA CARBOXYLASE ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                  MITOCHONDRION (POTENTIAL).
                                                                                                                                                              251CACF6464B046B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-biotin-containing subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                     DB 1;
.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              that shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leaves, flowers
                                                                                                                                                              CRC64;
                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              due
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCO(3)(-) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to erroneous
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                                                                                                        0;
                                                                                                     Gaps
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RESULT 10
PYCB_METTH
InterPro; IPRO01882; Biotin_attacl
InterPro; IPR000089; Biotin_lipoyl
InterPro; IPR000891; HMGL-like.
InterPro; IPR000891; PYC_OADA.
Pfam; PP00364; biotin_lipoyl; 1.
Pfam; PF00682; HMGL-like; 1.
Pfam; PF00436; PYC_OADA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000
30-MAY-2000
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Purification, regulation, and molecular and biochemical characterization of pyruvate carboxylase from Methanobacterium thermoautotrophicum strain deltaH.";
J. Biol. Chem. 273:5155-5166(1998).
-I- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL GROUP TO PYRUVATE IN THE SECOND. THE MAXIMUM ACTIVITY IS AT PH 8 AND 60 DEGREES CELSIUS.
-I- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) - ADP + phosphate +
                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyruvate carboxylase subunit B (EC 6.4.1.1) (Pyruvic carboxylase PYCB OR MTH1107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                 TIGRFAMS; TIGRO1108; oada; 1. PROSITE; PS00188; BIOTIN; FALSE_NEG.
                                                                                                                                                                                                                                                                entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Delta H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYCB_METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mukhopadhyay B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98148063; PubMed=9478969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=187420;
                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                    ENZYME REGULATION: INHIBITED BY ADP AND ALPHA-KETOGLUTARATE. SUBUNIT: HETEROCCTAMER.OF FOUR A AND FOUR B SUBUNITS. SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: ATP, MAGNESIUM (OR MANGANESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oxaloacetate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BICARBONATE.
                                                                                                                                                                                                            AE000881;
AF039105;
                                                                                                                                                                                             P02905; 1BDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 39, Createa)
(Rel. 39, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD
                                                                                                                                                                                                            AAB85596.1; -.
AAC12719.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stoddard S.F.,
                                                                                                                                      Biotin_lipoyl.
HMGL-like.
                                                                                                                                                                         Biotin_attach.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wolfe R.S.;
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R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COBALT),
                                                                                                                                                                                                                                                                                                                                  restrictions
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                                                                                                                                                                                                                                                                                                                                                                   a collaboration
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Multifunctional

enzyme; Gluconeogenesis; Magnesium;

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BCCP_PORP
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Best Local
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                                                                                                                                                                                       Fatty acid biosynthesis; Biotin; Chloroplast.
BINDING 122 122 BIOTIN (BY SIMILARITY).
SEQUENCE 157 AA; 17519 MW; 5CFF079B2410E777 CRC64;
                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001882; Biotin_attach.
InterPro; IPR000089; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Rhodophyta; NCBI_TaxID=2787;
                                                                                                                                                                                                                                                                  TIGREAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U38804; AAC08169.1; -. HSSP; P02905; 1BDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Avonport; Reith M.E., Munholland J.;
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                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001249; AcCoA_biotinCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete nucleotide
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L5-JUN-2002 (Rel.
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                                            4 IPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKE 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE COMPLEX; FIRST, BIOTIN CARDXYLASE CATALYZES THE CARBITER PROTIN CARD THEN THE TRANSCARBOXYLASE CATALYZES THE CARRITER PROTIN AND THEN THE TRANSCARBOXYLASE TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European
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IVSPMVGTFYHSPAPGEKIFVQVGDIVKCNQTVCIIEAMKLMNEIEAEIEGIIIEILVKN 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an email to license@isb-sib.ch).
                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                 PR01071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                               PS00188; BIOTIN; 1
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534
568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Long-chain fatty acid biosynthesis; first step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                               ACOABIOTINCC.
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41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                    40.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of the Porphyra purpurea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13:333-335(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein of acetyl-CoA carboxylase (BCCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥.
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                                                                                                                       Pred. No.
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Pred. No. 8.
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BIOTIN.
BJ328715AB0328DBB CRC64;
                                                                                                                                        Score 138.5;
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                                                                                              Mismatches
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                                                                                                                    3.1e-07;
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.1e-07
                                                                                                                                           DB 1;
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                                                           EMBL; X59890; CAA42544.1;
EMBL; Z36087; CAA65182.1;
EMBL; U35647; AAC49147.1;
PIR; S46094; S46094.
HSSP; P24182; IBNC.
SGD; S0000422; PYC2.
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Dubois E., e
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P32327;
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem.
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01-OCT-1994 (Rel. 30,
15-JUL-1999 (Rel. 38,
                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                 the European Bioinformatics Institute. There are no resiuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                       effects on protein biotinylat Biochem. J. 312:817-825(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=96128067; Val D.L., Chapman-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pyruvate carboxylase-deficient strains.";
Mol. Gen. Genet. 229:307-315(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "DNA sequences in chromosomes II and VII code for pyruvate carboxylase isoenzymes in Saccharomyces cerevisiae: analys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae; Saccharomycetaceae; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Last annotation update) Pyruvate carboxylase 2 (EC 6.4.1.1) (Pyruvic PYC2 OR YBR218C OR YBR1507.
                                                                                                                                                                       entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wallace J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stucka R., Dequin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND CHARACTERIZATION MEDLINE-92017667; PubMed-1921979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
           InterPro;
                        InterPro;
                                     InterPro;
                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Polymorphism of the yeast pyruvate carboxylase effects on protein biotinylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                             SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                            INDUCTION: BY GLUCOSE. SIMILARITY: WITH OTHER
                                                                                                                                                                                                                                                                                                                 COFACTOR: BIOTIN AND ZINC PATHWAY: GLUCONEOGENESIS. SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ATP
                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL GROUP TO PYRUVATE IN THE SECOND.
                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                           oxaloacetate.
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                                  IPR001882;
IPR000089;
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           IPR000891;
                       IPR000901;
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                                                                                                                                                                     license agreement
                       CPSase.
                                  Biotin_lipoyl.
         HMGL-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Walker M.E., Cronan J.E. Jr.,
                                                                                                                                                                                                                                                                                                                                                                       pyruvate
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CPSase_L_chain;
biotin_lipoyl;

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Best Local S
Matches 25
                                                                                                                                                                                               PYC1_YEAST
P11154;
01-JUL-1989
01-OCT-1996
15-JUL-1999
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PROSITE; E
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SEQUENCE FROM N.A.
STRAIN-S288C;
                                                                      MEDLINE-8829805; pubMed-3042770; Mallace J.C.; Lim F., Morris C.P., Occhiodoro F., Wallace J.C.; "Sequence and domain structure of yeast pyruvate carboxylase."; J. Biol. Chem. 263:11493-11497(1988).
                                                                                                                                                                             01-OCT-1996 (Rel. 34, L
15-JUL-1999 (Rel. 38, L
Pyruvate carboxylase 1
PYC1 OR PYV OR YGL062W.
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                                                                                                                                              Eukaryota; Fung1;
Saccharomycetales;
                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                    NCBI_TaxID=4932;
                                                                                                                 EQUENCE FROM N.A.,
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PF00364;
PF00682;
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                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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1001
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1180
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(Rel. 34, Last seq
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CPSase_L_D2; 1.
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                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family
                                                                                                                                              Ascomycota; Saccharomycotina; Sacc; Saccharomyces;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1180
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                                                                                                                 AND PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                        40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                       130166
                                                                                                                                                                                      Last sequence update)
Last annotation updat
1 (EC 6.4.1.1) (Pyruvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme; Biotin; Gluconeogenesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).

BY SIMILARITY.

BIOTIN (BY SIMILARITY).

CARBAMOYL PHOSPHATE SYNTHETASES.

WITH OTHER BIOTIN CARROXYLASES.

WITH LIPOAMIDE ACETYLTRANSFERASE.

S -> C (IN REF. 1).

D -> E (IN REF. 1).

N -> K (IN REF. 1).

L -> F (IN REF. 1).

S -> C (IN REF. 1).

GTA -> STR (IN REF. 1).

GTA -> STR (IN REF. 1).

GTA -> STR (IN REF. 1).

GTA -> STR (IN REF. 1).

GTA -> STR (IN REF. 1).

Y -> N (IN REF. 1).

Y -> N (IN REF. 1).

X -> P (IN REF. 1).

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9; Mismatches
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                                                                                                                 SEQUENCE.
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                                                                                                                                                                                       on update)
(Pyruvic (
                                                                                                                                                                                                                                          1178
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2.7e-06;
21;
                                                                                                                                                                                       carboxylase 1) (PCB
                                                                                                                                                       Saccharomycetes;
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 cerevisiae
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Query Match
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SIMILAR
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PROSITE; F
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"Yeast pyruvate carboxylase: gene isolation.";
Biochem. Biophys. Res. Commun. 145:390-396(1987).
-i- punction: pyruvate CARBOXYLASE CATALYZES A 2-STEP R
-INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE CO
                                                                                                                                                                                                                                                                                               Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J03889; AAA34
EMBL; Z72584; CAA96
PIR; A29233; QYBYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute use by non-profit institutions as 1 modified and this statement is not rem
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[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosomes.";
Yeast 13:861-869(1997).
                                                                                           CONFLICT
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                                                                                                                                                       SIMILAR
                                                                                                                                                                                              NP_BIND
                                                                                                                                                                                                         Zinc;
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                                                                                                                                                                                                                                                                                                                     Pfam;
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                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-87241529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1003-1178 FROM N.A.
                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                   ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: BIOTIN AND ZINC.
PATHWAY: GLUCONEOCENESIS.
SUBUNIT: HOMOTETRAMER.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES,
AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oxaloacetate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOXYL GROUP TO PYRUVATE IN THE SECOND
                                                                                                                                                                                                                                                                                                                                                                                 S0003030;
                                                                                                                                                                                                                                                                                               PF00364;
PF00682;
                                                                                                                                                                                                        Multigene
                                                                                                                                                                                                                                                                                                                     PF00289;
                                                                                                                                                                                                                   Multifunctional
                                                                                                                                                                                                                                            PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                            ; IPR000089; 1; IPR000901; (; IPR000891; 1; IPR003379; 1
                                                                                                                                                                                                                           PS00866; CPSASE_1; PS00867; CPSASE_2;
                                         462
493
595
619
664
772
879
909
1178
                                                                                                                                                                                                                                                                                                                                                                                                              AAA34843.1;
CAA96765.1;
                                                                                                                                                                                                                                                         CPSase_L_D2;
)1235; pyruv_
                                                                                                                                                                                                                                                                            Biotin_carb_C;
                                                                                                                                                                                                                                                                                                HMGL-like;
                                                                                                                                                                                                                                                                                                           biotin_
                                                                                                                                                                                                                                                                                                                     03379; PYC_OADA.
CPSase_L_chain; 1.
                                                                                                                                                                                                                                                                                       PYC_OADA;
                                        ₽
K
                                                                                                                                                                                              family.
187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=3036126;
          38.9%;
42.2%;
                                                                                                                                                                                                                                                                                                                                                   Biotin_lipoyl.
CPSase.
                                                                                                                                                                                                                                                                                                                                         HMGL-like.
                                                                                                                                                                                                                                                                                                                                                                      Biotin_attach.
                                         130099
                                                                                                                                                                                                                                                                                                         lipoyl;
                                                                                                                                                                                                                  enzyme;
Score 133; DE
Pred. No. 8.5e
L5; Mismatches
                                        Ma
No⊞
                                                                                                                                                                                                                                                                                                                                                                                                                                                               is not removed.
                                                                                                                                  WITH
HTIW
WITH
                                                                                                                                          CARBAMOYL PHOSPHATE SYNTHETASES. WITH OTHER BIOTIN CARBOXYLASES. WITH OTHER BIOTIN CARRIER PROTEINS
                                                                               ១ខេ
                                                                                                                                                                          BIOTIN
                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pyruvate + HCO(3)(-) - ADP + phosphate
                                                                                                                                                                                                               Biotin;
                                                                                                            LIPOAMIDE ACETYLTRANSFERASE
G (IN REF. 1).
D (IN REF. 1).
                                         BC7110A8AFB23E04
                                                                              (IN REF.
(IN REF.
(IN REF.
(IN REF.
                                                                                                                                                                          (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         long
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                Gluconeogenesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are
                                                                       REF.
DB 1; 1; 5e-06; les 22;
                                                            REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2-STEP REACTION, OF THE COVALENTLY TRANSFER OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIPOAMIDE TRANSFERASES
                   Length 1178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ņ
                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                n no way
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Matches

Similarity 27; Conserv

Conservative

15;

Indels

0

Gaps

0,

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RESULT 14
PYC_PICPA
       SOFT TO THE REPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                     Interpro; IPR000901; CPSase.
Interpro; IPR000891; HMGL-like.
Interpro; IPR003891; PYC_OADA.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF00364; biotin_lipoy1; 1.
Pfam; PF003682; HMGL-like; 1.
Pfam; PF00245; PYC_OADA; 1.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF02786; CPSase_L_D2; 1.
    ACT_SITE
BINDING,
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYC_PICPA
P78992;
01-NOV-1997
                                                                                                                                        TIGRPAMS; TIGRO1235; PYTUV_carbox; PROSITE; PS00188; BIOTIN; 1. PROSITE; PS00866; CPSASE_1; 1. PROSITE; PS00867; CPSASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y11106; CAA71993.1;
HSSP; P24182; 1DV1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (eor send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98301182; PubMed=9639311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pichia pastoris (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyruvate
                                                                                                                  ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (east
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     St 14:647-654(1998).

FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE COVALENTLY ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL GROUP TO PYRUVATE IN THE SECOND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oxaloacetate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLLV 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGLI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001882; Biotin_attach.
       185
315
1140
1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLUCONEOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOTIN AND ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
       AA,
                         1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ascomycota; Saccharomycotina; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35,
                                                 \frac{190}{315}
                                                                                                                                                                                                                                                                                                                                                                                                                                   Biotin_lipoyl.
       131400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 6.4.1.1) (Pyruvic ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence
                                                                                                                     enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP
       Œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agreement (See
ATP (POTENTIAL).
BY SIMILARITY.
BIOTIN (BY SIMILARITY).
WW.; 8B6E858079657914 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pyruvate
                                                                                                                Biotin; Gluconeogenesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Pyruvic carboxylase) (PCB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECOND (BY SIMILARITY)
e + HCO(3)(-) = ADP + F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyruvate
e pyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCCA_MYCLE
P46392;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21128732; PubMed-11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Whoseler P.R., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Oglail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOY-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40; Last sequence update)
15-UNT-2002 (Rel. 41, Last annotation update)
Acetyl-/propionyl-coenzyme A carboxylase alpha chain [Includes: Biotin carboxylase (EC 6.3.4.14); Biotin carboxyl carrier protein (BCCP)].
BCCA OR ML0726 OR B1308_C1_129.
                                                                                                                                                                                                                                                                                                                                                      Nature 409:1007-1011(2001).
-I- FUNCTION: THIS PROTEIN CARRIES TWO FUNCTIONS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carboxyl carrier protein tuberculosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1107 EIGAPMAGVVVEVRVHENGEVKKGDPIAVLSAMKMEMVISSPVAGRIGQIAVKENDSV 1164
                                                                                                                                                                                                                                                                                                                                                                                                        Squares S., S
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Smith D.R., Robison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Norman E., de
Dale J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales;
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                       "Massive gene decay in the leprosy bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Lipid synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV
                                                                                                                                                                                                                                                                                  CARRIER PROTEIN AND BIOTIN CARBOXYLTRANSFERASE.

CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)

ADP + phosphate + carboxybiotin-carboxyl-carrier protein.

COFACTOR: BIOTIN.
                                                                                                                                                                                   AND SUBSTRATE BINDING ACTIVITY. SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES
                                                                                                                                                                                                              PATHWAY: Long-chain fatty acid biosynthesis; first step. SUBUNIT: MULTIMER COMPRISED OF 2 DIFFERENT SUBUNITS; THE ONE (63/64 kDa) HAS BIOTIN CARBOXYLASE AND BIOTIN CARRIER FUNCTIONS, WHILE THE SMALLER SUBUNIT POSSESSES CARBOXYLTR.
                                                                                                                                                                    PHOSPHATE SYNTHETASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MAR-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176:2525-2531(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=7909542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K.A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ...
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mycobacteria: characterization of the biotin
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Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF02786; CPSase_L_D2; 1.
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Q42777; Q42778;
15-JUN-2002 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-cv. Corsoy MEDLINE-94286521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta; eurosids I; Fabales; Fabaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max (Soybean)
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                                                                                                                                                                                                                                                                                                                     domains.
                                                                                                                                                                                                                                                                                                                                           Song J., Wurtele E.S., Nikolau B.J., "Molecular cloning and characterization of the cDNA coding "Molecular cloning and characterization of the cDNA carboxyl biotin-containing subunit of 3-methylcrotonoyl-CoA carboxyl identification of the biotin carboxylase and biotin-carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
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                                                                                                                                                                              C. Natl. Acad. Sci. U.S.A. 91:5779-5
CATALYTIC ACTIVITY: ATP + 3-methylc
phosphate + 3-methylglutaconyl-CoA.
COFACTOR: Bottin.
                                PATHWAY: Leucine catabolism.
SUBUNIT: Probably a heterodimer composed of biotin alpha subunits and beta subunits (By similarity).
SUBCELLULAR LOCATION: Mitochondrial matrix.
TISSUE SPECIFICITY: In leaves, cotyledons and stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG
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IPR000901; CPSase
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9; TISSUE=Cotyledon;
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Pred. No. 8
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                                                                                                                                                                                                                                                 91:5779-5783(1994).
3-methylcrotonyl-CoA
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                                      and stems
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eudicots; Rosic
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Matches 29
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InterPro; IPR00089; Biotin_lipoyl.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000901; CPSase_C; 1.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF02786; CPSase_L_D2; 1.
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Zhang J., Xia W.L., Brew K., Ahmad F.;
Zhunded Carboxylase: amino acid sequence and domain structure deduced from cDNA sequencing.";
Zhoc. Natl. Acad. Sci. U.S.A. 90:1766-1770(1993).

-i- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TIS SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KI
                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pyruvate carboxylase, mitochondrial precursor
                                                                                                                                                                                        TISSUE-Adipocyte;
MEDLINE-93189578; PubMed-8446588;
Ahma
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                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                          carboxylase) (PCB).
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PS00866; CPSASE_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 email to license@isb-sib.ch).
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AAA53141.1;
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Rodentia;
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BY SIMILARITY.

BIOTIN (BY SIMILARITY).

R -> K (IN REF. 1; AAA5:

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Pred. No. 1.1e
L2; Mismatches
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Sciurognathi; Muridae;
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l.le-05;
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Murinae; Mus
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      KIDNEY)
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Pfam; PP00299; CPSase_L_chain; 1.
Pfam; PP00364; blotin_lipoyl; 1.
Pfam; PP00682; HMGL-11ke; 1.
Pfam; PP02456; PYC_OADA; 1.
Pfam; PP02785; Blotin_carb_C; 1.
Pfam; PP02786; CPSase_L_D2; 1.
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InterPro; IPR000089; I
InterPro; IPR000901; I
InterPro; IPR000891; I
 BCCP_ANASP STANDARD; PRT; 181 AA. 005881; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Biotin carboxyl carrier protein of acetyl-CoA ACCB OR ALL5057.
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HSSP; P24182; 1BNC.
SWISS-2DPAGE; Q05920; MOUSE.
MGD; MGI:97520; Pcx.
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ATP-binding;
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COFACTOR: BIO
PATHWAY: GLUC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collable een the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                    EGDDLILEI 1177
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                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                 Similarity 40.0
28; Conservative
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ling; Mitochondrion; Lipid synthesis; Transit peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLUCONEOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOTIN AND MANGANESE
                                                                                                                                                           69
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                                                                                                                                                                                                                                                                                           203
328
1144
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1178
549
1000
1178
                                                                                                                                                                                                                                                                                                                                                                                                                            35; pyruv_carbox; 1.
BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                          37.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biotin_attach.
Biotin_lipoyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPSase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HMGL-like.
                                                                                                                                                                                                                                                                                 129684
                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOTIN CARBOXYLASES, SYNTHETASES.
                                                                                                                                                                                                                                                                               (BY SIMILARITY).
AIP (BY SIMILARITY).
BY SIMILARITY.
BIOTIN (BY SIMILARITY).
MW; 14CEAOF9DA8B8127 CRC
                                                                                                                                                                                                                               Score 129; DB 1;
Pred. No. 2.1e-05;
4; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                         BIOTIN CARBOXYLASE (BY SIMILARITY).
CARBOXYLTRANSFERASE (BY SIMILARITY).
BIOTIN CARBOXYL CARRIER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND
                                                                                                                                                                                                                                                                                                                                                                               PYRUVATE CARBOXYLASE
                                                                                                                                                                                                                                                                                                                                                                                          MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pyruvate
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            acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRAIN) SYNTHESIS FROM PYRUVATE
e + HCO(3)(-) = ADP + phosphate
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            carboxylase (BCCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE,
                                                                                                                                                                                                                                                       Length 1178;
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                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                 Indels
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tions on its
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RESULT 19
BCCA_MYCTU
ID BCCA_M
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DE ACETY1
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Best Local :
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HSSP; P02905; 1BDO.

InterPro; IPR001249; AcCoA_biotinCC.

InterPro; IPR001882; Biotin_attach.

InterPro; IPR000889; Biotin_lipoyl.

Pfam; PF00364; biotin_lipoyl; 1.

PRINTS; PR01071; ACOABIOTINCC.

TIGRFAMS; TIGR00531; BCCP; 1.
                       BCCA_MYCTU
P46401;
01-NOV-1995
01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                              INIT_MET
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
"Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8.205-213(2001).

-I- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES. THE CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES. THE CARBOXYLASION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE THE CARROXYLAGROUP TO FORM MALONYL-COA.
          01-NOV-1995 (Rel. 32, Creat 01-NOV-1995 (Rel. 32, Last 15-JUN-2002 (Rel. 41, Last Acetyl-/propionyl-coenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., K. Kishida Y., Kohara M., Matsumoto M., Matsuno A., Murak Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 1-9.

MEDLINE-93352435; PubMed-8102363;
Gornicki P., Scappino L.A., Haselkorn R.;
"Genes for two subunits of acetyl coenzyme A carboxylase of Anabaena sp. strain PCC 7120: biotin carboxylase and biotin carboxyl carrier protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L14863; AAA74628.1; -. EMBL; AP003598; BAB76756.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entitles requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales;
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                          Fatty acid biosynthesis; Biotin; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00188; BIOTIN;
                                                                                                                                                                                                                            105
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                                                                                                                                                                                              56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content if the statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol. 175:5268-5272(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: Long-chain fatty acid biosynthesis; first step SUBUNIT: HOMODIMER.
                                                                                                                                                                 NGEPVEYNQPLMRI
                                                                                                                                                                                           ERDAVQGGQGLIKI
                                                                                                                                                                                                                         EIPAPLAGTVSK-----ILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK
                                                                                                                                                                                                                                                                                     Similarity
26; Conserv
                                                                                                                                                                                                                                                                                                                                                145
181 AA;
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                                                                                       STANDARD;
. 32, Createu,
32, Last sequence upd.
1. 41, Last annotation u
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19049
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                                                                                                                                                                                                                                                                                                    37.0%;
35.1%;
                                                                                                                                                                                                                                                                                                                                                  MW.
                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                     Score 126.5;
Pred. No. 5.8e
19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                EBEC7B16CDC8225F
                                           update)
                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
7B16CDC8225F CRC64;
          update)
ase alpha
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ies 22;
                                                                                       B
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a K., Kimura
, Muraki A.,
                                                                                                                                                                                                                                                                                                                  Length 181;
                                                                                                                                                                                                                                                                                     Indels
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carboxylase

chain

[Includes:

Biotin

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EMBL;
EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Stulston J.E., Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dale J.W.;
"Lipid synthesis in mycob carboxyl carrier protein tuberculosis.";
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White C
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzbe
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Miku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=CDC 1551 /
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[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94222829; PubMed=7909542; Norman E., de Smet K.A.L., Stoker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                       TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases -1- FUNCTION: THIS PROTEIN CARRIES TWO FUNCTIONS: BIOTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98295987;
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                             InterPro;
                                                                                      TubercuList; Rv2501c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTIONS, WHILE THE SMALLER SUBUNIT POSSESSES CARBOXYLTRANS AND SUBSTRATE BINDING ACTIVITY.
SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: MULTIMER COMPRISED OF 2 DIFFERENT SUBUNITS, THE ONE (63/64 kDa) HAS BIOTIN CARBOXYLASE AND BIOTIN CARRIER FUNCTIONS, WHILE THE SMALLER SUBUNITE DOSCROOMS

    ADP + phosphate + carboxybiotin-carboxyl-carrier
COFACTOR: BIOTIN.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARRIER PROTEIN AND BIOTIN CARBOXYLTRANSFERASE.

CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHATE SYNTHETASES.
                                                                                                                                      ; Z19549; CAA79609.1;
; Z95556; CAB08919.1;
; AE007094; AAK46880.1;
; P24182; 1BNC.
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                                                                                                              MT2576;
IPR001882;
IPR000089;
IPR000901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176:2525-2531(1994)
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; Biotin_attach.
; Biotin_lipoyl.
; CPSase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOXYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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Best Local
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084125;
16-0CT-2001
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
Pfam;
Pfam;
                                                                                                            use by non-profit institumodified and this statement entitles requires a license
                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                            "Genome sequence of an ob
Chlamydia trachomatis.";
Science 282:754-759(1998)
                                                                                                                                                                                                                                                                                                      MEDLINE-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao
                                                     EMBL; AE001286; AAC6
HSSP; P02905; 3BDO.
PHCI-2DPAGE; 084125;
                                                                                                  or send an email to license@isb-sib.ch;
                                                                                                                                                                                                                                                                                                                                           STRAIN-D/UW-3/Cx;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis. Bacteria; Chlamydiales;
                                                                                                                                                                                                                                                                                                                                                                                                              ACCB or CT123
                                                                                                                                                                                                                                                                                                                                                                                                                         Biotin carboxyl carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00867; CPSASE_2; 1.
Fatty acid biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       646 EQVLARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          w
                                                                                                                                                                                                              FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL CARBOXYLASE CAPALY. FIRST, BIOTIN CARBOXYLASE CATALY CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRATERANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA (BY
                                                                                                                                                                                          PATHWAY: Long-chain fatty acid biosynthesis; first SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQGLIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVVSPMPGSVIAVQVESGSQISAGDVVVVVVEANKMEHSLEAPVSGRVQ-VLVSVGDQVKV 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  588
162
294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 40, Created)
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Biotin_carb_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPSase_L_D2;
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                                                                             AAC67714.1;
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167
294
620
70592
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                                                                                                                                   institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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BY SIMILARITY.
BIOTIN (BY SIMILARITY).
FAAOALB46432CABF CRC64;
                                                                                                             agreement
                                                                                                                       is not removed.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                       of acetyl-CoA
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                                                                                                                                                                                                                                                                                                                                                                                                                        carboxylase (BCCP).
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                                                                                                                                                       outstation
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InterPro; IPR001249; ACCOA_bia InterPro; IPR001882; Biotin_ai InterPro; IPR000189; Biotin_li Pfam; PF00364; biotin_lipoy1; PRINTS; PR01071; ACOABIOTINCC

Biotin_lipoyl. Biotin_attach Accoa_biotincc

SQ

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В.Н.

Greenberg

C.R.,

associated with

two

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Query Match
Best Local S
Matches 30
                                                                                 MEDLINE-85030380; PubMed-6548474;
Freytag S.O., Collier K.J.;
"Molecular cloning of a cDNA for human pyruvate carboxylase.
Structural relationship to other biotin-containing carboxylases regulation of mRNA content in differentiating preadipocytes.";
J. Biol. Chem. 259:12831-12837(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                   Carbone
                              VARIANTS PC DEFICIENCY THR-610 AND ILE-743.
MEDLINE-98254451; PubMed-9585612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Kidney;

MEDLINE=94324922; PubMed=8048912;

Mackay N., Rigat B., Douglas C., Chen H.S., Robinson B.H.;

"cDNA cloning of human kidney pyruvate carboxylase.";

"cDNA cloning of human kidney pyruvate carboxylase.";
                                                                                                                                                                                                                            SEQUENCE OF 1135-1178 FROM N.A.
                                                                                                                                                                                                                                                              MEDLINE-87212051; PubMed-3555348;
Lamhonwah A.-M., Quan F., Gravel R.A.;
"Sequence homology around the biotin-binding propionyl-CoA carboxylase and pyruvate carbox Arch. Biochem. Biophys. 254:631-636(1987).
                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1083-1178 FROM MEDLINE-87212051; PubMed-35 Lambonwah A.-M., Quan F., G
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Liver, and Kidney; Walker M.E., Jitrapakdee Submitted (JUL-1995) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGREAMS; TIGRO0531; BCCP; 1.

PROSITE; PS00188; BIOTIN; 1.
Fatty acid biosynthesis; Biotin; Complete proteome.
BINDING 128 128 BIOTIN (BY SIMILARITY).

164 AA: 18198 MW; BD0BA4CEBC2D384C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim. Biophys. Acta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Primary amino acid sequence and
carboxylase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver, and Kidney; MEDLINE-95002202; Pubmed-7918683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, 15-JUN-2002 (Rel. 41, Pyruvate carboxylase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P11498; Q16;
01-OCT-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         er I.D., Du Y., Lisgaris M.V., Mandal S.K., B.-S., Liu T.-C., Kwon M., Patel M.S., Kern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRVEEILITNGDPVQFGSKLFRI 161
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                 M.A.,
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               MacKay N.,
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Primates;
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36.1%;
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Last annotation update)
mitochondrial precursor
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             Ling M.,
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EMBL/GenBank/DDBJ databases.
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 122;
Pred. No. 1.
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        Cole D.E.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     structure of
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.5e-05;
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        Douglas C.,
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        Rigat B.,
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS.
-I- SUBUNIT: HOMOTETRAMER.
-I- SUBCELLULAR LOCATION: Mitochondrial matrix.
-I- DISEASE: DEFICIENCY IN PC CAUSES LACTIC ACIDOSIS, MENTAL RETARDATION AND DEATH. OCCURS IN THREE FORMS: TYPE A (MILD); TYPE B (SEVERE NEONATAL) AND A VERY MILD LACTICACIDEMIA.
-I- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                     Ligase; Multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY) AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.
-I- CATALYTIC ACTIVITY: ATP + PYRUVATE + HCO(3)(-) = ADP + phosphate
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Seargeant L., Robinson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; U04641; AAA99537.1; -...; S72370; AAB31500.1; -...; U30891; AAA82937.1; -...; M26122; AAA36423.1; -...; K02282; AAA60033.1; -...
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S01469; S01469.
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PF00682; HMGL-like; 1.
PF02436; PYC_OADA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pro; IPR000901; CPSase.
Pro; IPR000891; HMGL-like.
Pro; IPR003379; PYC_OADA.
PF00289; CPSase_L_chain; 1.
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                                                                                                                                                                                                                                                                                                                                           mutation.
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328
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Biotin_lipoyl.
CPSase.
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(See http://www.isb-sib.ch/announce/

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Lipid synthesis;

Biotin; Manganese; Gluconeogenesis; id synthesis; Transit peptide;

BIOTIN CARBOXYL CARRIER

(BY SIMILARITY)

BY SIMILARITY.

(BY SIMILARITY).

PYRUVATE CARBOXYLASE.
BIOTIN CARBOXYLASE (BY SIMILARITY)
CARBOXYLTRANSFERASE (BY SIMILARITY)

SIMILARITY)

MITOCHONDRION (POTENTIAL).

BIOTIN (BY SIMILARITY).

A -> T (IN PC DEFICIENCY TY
/FTId=vAR_008095.

M -> I (IN PC DEFICIENCY TY
/FTId=vAR_008096.

LA -> WP (IN REF. 2).

A -> S (IN REF. 3).

RS -> PT (IN REF. 2).

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                                              use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                   STRAIN-Wistar; TIS
MEDLINE-96257760;
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"The
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyruvate carboxylase, mitochondrial carboxylase) (PCB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             P52873: 064555;
01-0CT-1996 (Rel. 34, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                             entities requires a license agreement (some send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata;
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                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                      PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS.
SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: MITOCHORITAL MATTIX.
SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES,
AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                         oxaloacetate.
COFACTOR: BIOTIN AND MANGANESE
                                                                                                                                                                         FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY) AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE. CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) - ADP + phosphate
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  U32314;
U36585;
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  AAA96256.1;
AAC52668.1;
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Booker G.W., Cassady A.I., Wallace
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Pred. No. 0.00014;
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P -> R (IN REF. 2).
E -> A (IN REF. 2).
DT -> AP (IN REF. 2).
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                                         use by non-profit institutions as lon modified and this statement is not removentitles requires a license agreement (so or send an email to license@isb-sib.ch).
                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                        STRAIN-ATCC 700084 / mc(2)155;
MEDLINE-99328972; PubMed-10400584;
MEDLINE-99328972; PubMed-10400584;
MEDLINE-99328972; PubMed-10400584;
MEDLINE-99328972; PubMed-10400584;
MEDLINE-99328972; PubMed-10400584;
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MEDLINE-99328972; PubMed-10400584;
MEDLINE-9932897289728972;
MEDLINE-99328972; PubMed-10400584;
MEDLINE-993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium smegmatis.
Mycobacterium smegmatis.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Bacteria; Actinobacterineae; Mycobacteriaceae; Mycobacterium
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InterPro; IPR003379;
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PF00682; HMGL-like; 1.
PF02436; PYC_OADA; 1.
PF02785; Biotin_carb_C; 1.
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CARBOXYLTRANSFERASE (BY SIMILARITY).
BIOTIN CARBOXYL CARRIER PROTEIN
(BY SIMILARITY).
ATP (BY SIMILARITY).
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P -> S (IN REF. 2).
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                                                                                              Usage
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STRAIN=MOPN / Nigg;

STRAIN=MOPN / Nigg;

MEDLINE=20150255; PubMed=10684935;

MEDLINE=20150255; PubMed=10684935;

Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg Read T.D., Brunham R.C., Peterson J., Utterback T., Berry White O., Hickey E.K., Peterson J., Utterback T., Berry White O., Hickey E.K., Peterson J., Craven B., Bowman C., Tahan K., Weidman J., McClarty G., Weidman J., McClarty G., McClarty G., Rolonay J., McClarty G., McCl
                                                                InterPro; IPR001249; AcCoA_biotinCC InterPro; IPR001882; Biotin_attach. InterPro; IPR001089; Biotin_lipoyl. InterPro; IPR001089; Biotin_lipoyl. Pfam; PF00364; biotin_lipoyl; 1.prints; PR01071; AcoaBioTincc.
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16-OCT-2001
16-OCT-2001
                          TIGRFAMS; TIGR00531; BCCP; PROSITE; PS00188; BIOTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids Res. 28:1397-1406(2000).

-I- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA (By similarity).
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HSSP; P02905; 1BDO.
TIGR; TC0399; -.
                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
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Bacteria; Chlamydiales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
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15-JUN-2002 (Rel. 41, Last annotation updat
Biotin carboxyl carrier protein of acetyl-C
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Pro; 1PR001882;
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                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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ACEF OR ACEB OR PA5016.
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MEDLINE-20437337; PubMed-
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Q59638;
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15-JUN-2002 (Rel. 41, Last annotation update)
Dihydrolipoamide acetyltransferase component
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                                                                                                                                                                  acetyldihydrolipoamide.
COFACTOR: THE E2 COMPONENT
COFACTORS (BY SIMILARITY).
SUBUNIT: FORMS A 24-POLYPE
                                                                                                                                                                                                                      lipoamide dehydrogenase (E3).
CATALYTIC ACTIVITY: Acetyl-CoA
                                                                                                                                                                                                                                                 FUNCTION: The pyruvate dehydrogenase complex catalyzes the conversion of pyruvate to acetyl-coA and CO(2). It contains multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2)
                                                                 European Bioinformatics Institute.
                                                                                                                          SIMILARITY:
                                                                                                                                      SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGE-IPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
             an
          non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹,
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                                                                                                                       CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed-10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 I
18084 MW;
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                                                                                                                                                                   24 - POLYPEPTIDE
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                                                                                                            TO THE 2-OXUACID DUMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lamont I.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOTIN (BY SIMILARITY).
; 8536D58B5CE11D3B CRC64;
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                                                                                                                                      2-OXOACID DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subdivision;
                                                                                                                                                                                                                      + dihydrolipoamide = CoA
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No. 3
                                                                                                                                                                STRUCTURAL CORE WITH OCTAHEDRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              547
                                                 There are no restrictions ong as its content is in
                                                                                                                                                                                             TWO COVALENTLY - BOUND LIPOYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
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Lim R.M.,
                                                                                                                                                                                                                                                   (E2)
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Best Loc
Matches
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BTB7_MYCTU
                  SEQUENCE FROM WILL.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L.,
Fleischmann R.D., Alland D., Eisen J.A., Famolaeva M.D.,
Fleischman J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
Kolonay J.F., Nelson W.C., Umayam I.A., Khouri H., Gill
                                                                                                                Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harri Gordon S.V., Eiglmeder K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyo Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.; Nature 393:537-544(1998).
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BINDING
ACT_SITE
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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EMBL;
HSSP;
                                                                                                                                                                                                                          MEDLINE=98295987;
Cole S.T., Brosch
Gordon S.V., Eiglm
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Interpro; IPRO03016; Lipoyl.
Pfam; PF00198; 2-oxoacid_dh; 1.
Pfam; PF00364; biotin_lipoyl; 2.
Pfam; PF002817; e3_binding; 1.
                                                                                                                                                                                                                                                                                                                                               Biotinylated protein TB7.3. RV3221C OR MT3317 OR MTCY07D11.05
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 STRAIN-H37Rv;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              Actinomycetales;
                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis
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16-OCT-2001
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InterPro; IPR000089; Biotin_lipoyl.
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         Whole genome comparison
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AE004914;
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547 AA;
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PS00189; LIPOYL; 2.
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4; AAG08401.1;
                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                               Corynebacterineae;
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37.5%;
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           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acyltransferase;
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Pred. No. 0.00
14; Mismatches
           Mycobacterium tuberculosis
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GGAGATG -> AVPAPR (
MQ -> IE (IN REF. 1
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LIPOYL (BY SIMILARITY).
POTENTIAL.
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on update)
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                                J.,
           clinical and
                                                        White O., Hickey E.,
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                                           Salzberg
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Best Local (
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Q49110;
30-MAY-2000 (Rel. 3
30-MAY-2000 (Rel. 3
30-MAY-2000 (Rel. 3
                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Last sequence update)
Dihydrolipoamide acetyltransferase component (CCC 2.3.1.12) (E2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biotin; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prosite;
                  PYTUVATE METABOLISM IN MYCOPLASMA CAPTICOLUM.";

PTOTEIN SCI. 5:1719-1736(1996).

-I- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL

CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE

COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1),

DIHYDROCLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE

(E3) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Comparative evaluation of low-molecular-mass Mycobacterium tuberculosis identifies members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skjot R.L., Oettinger
                                                                                                                                                                                   Zhu P.P., Peterkofsky A.
                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=97001869;
                                                                                                                                                                                                                                                                                    Entomoplasmataceae
                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                        Mycoplasma
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InterPro; IPR000089; Biotin_lipoyl.
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MEDLINE-20072687;
                                                                                                                                                                                                                                                              NCBI_TaxID=2095;
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                                                                                                                                                              Sequence and organization of genes
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P10802; 1IYU.
MT3317; -.
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rE; PS00188; BIOTIN; FALS
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InterPro; IPRO04167; E3_binding.
InterPro; IPRO04167; E3_binding.
InterPro; IPRO03016; Lipoyl.
InterPro; IPRO03016; Lipoyl; 1.
Pfam; PF00198; 2-oxoacid_dh; 1.
Pfam; PF002617; e3_binding; 1.
ProDom; PD001115; 20xoacid_dh; 1.
PROSITE; PS00189; LIPOYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1998 (Rel. 07, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Dihydrolipoamide acetyltransferase component complex (EC 2.3.1.12) (E2).
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ACT_SITE
SEQUENCE
  Gregor J., Davis N.W., Mau B., Shao Y.;
"The complete genome so
                                                              Blattner F.R., Plunkett G. III, Bloch Kiley M., Collado-Vides J., Glasner J.
                                                                                                                                                                                                                     STRAIN-K12;
STRAIN-K12;
MEDLINE=83234434; PubMed=6345153;
Stephens P.E., Darlison M.G., Lewis H.M., Guest J.R.;
Stephens P.E., Darlison M.G., Lewis H.M., Guest J.R.;
"The pyruvate dehydrogenase complex of Escherichia co
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                                                                                                      SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                   Nucleotide sequence component.";
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Escherichia.
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COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALI
COFACTOR (BY SIMILARITY).
SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL COI
SYMMETRY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGI
SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.
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1C4T.
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Escherichia coli
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                                 , С.А.
J.D.,
i.A.,
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                                     .A., Perna N.T., Burl
., Rode C.K., Mayhew
, Goeden M.A., Rose I
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InterPro; IPR001078; 20xoacid_dh.
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InterPro; IPR003016; Lipoyl.
Pfam; PP00198; 2-oxoacid_dh; 1.
Pfam; PF00184; biotin_lipoyl; 3.
Pfam; PF002817; e3_binding; 1.
ProDom; PD001115; 20xoacid_dh; 1.

PIR; A30278; XXECDP. PIR; A16026; A16026. PIR; S45194; S45194. HSSP; P10802; 1DPC. SWISS-ZDPAGE; P06959;

EcoGene;

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EMBL; V01498; CAA24741.1; -. EMBL; D26562; BAA05573.1; -. EMBL; AE000120; AAC73226.1;
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                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91024917;
Ali S.T., Guest J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Amino acid sequence around lipoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K12 / EMG2;

MEDLINB=97443975; PubMed=9298646;

Link A.J., Robison K., Church G.M.;

"Comparing the predicted and observed p

in the genome of Escherichia coli K-12.

Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-12
STRAIN-K12 / EMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and characterization of domains of the E2p subunit of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               residue."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Russel G.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGENESIS OF HIS-602.
MEDLINE-90351365; PubMed-2201286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=84256520;
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                                                                                                                                                                                                                                                          SUBUNIT:
                                                                                                                                                                                                                                                                                             acetyldihydrolipoamide. COFACTOR: THE E2 COMPONENT CONTAINS
                                                                                                                                                                                                                                                                                                                           dehydrogenase (E1), dihydrolipoamide acetyltransferase
lipoamide dehydrogenase (E3).
CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide - CoA
                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: The pyruvate dehydrogenase complex catalyzes the conversion of pyruvate to acetyl-CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate
                                                                                                                                                                                                           SIMILARITY:
                                                                                                                                                                                                                          SIMILARITY:
                                                                                                                                                                                                                                              SYMMETRY.
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                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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Best Local S
Matches 32
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p14882;
p1-APR-1990 (Rel. 14, Created)
p1-DEC-1992 (Rel. 24, Last sequence update)
p16-OCT-2001 (Rel. 40, Last annotation update)
propionyl-CoA carboxylase alpha chain, mitochondrial precursor (EC 6.4.1.3) (PCCase alpha subunit) (Propanoyl-CoA; carbon diox)
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INIT_MET
                                                                                                                                                                                                                                                                                                                                                Browner M.F., Taroni F., Sztul E., Rosenberg L
Submitted (FEB-1989) to the EMBL/GenBank/DDBJ
-I- CATALYTIC ACTIVITY: ATP + propancyl-CoA +
phosphate + (S)-methylmalonyl-CoA.
-I- COFACTOR: BIOTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Browner M.F., Taroni F., Sztul E., Rosenberg L.E.;
"Sequence analysis, biogenesis, and mitochondrial import of alpha-subunit of rat liver propionyl-CoA carboxylase.";
J. Biol. Chem. 264:12680-12685(1989).
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Mammalia;
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MEDLINE-89308706; PubMed-2745462;
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                                                                           VATITY ACIDS, ISOLEUCINE, THREONINE, METHIONINE, AND VALINE.
SUBUNIT: PROBABLY A DODECAMER COMPOSED OF SIX BICTIN-CONTAINING
ALPHA SUBUNITS AND SIX BETA SUBUNITS.
SUBCELLULAR LOCATION: MILOCHONDRIAL MATTIX.
DISEASE: PROPIONIC ACIDEMIA DUE TO RECESSIVELY INHERITED
DEFICIENCY OF PCCASE ACTIVITY OFTEN CAUSES LIFE-THREATENING
KETOSIS AND ACIDOSIS.
                                                                                                                                                                                                                                                                                 COFACTOR: BIOTIN.

PATHWAY: KEY ENZYME IN THE CATABOLIC FATTY ACIDS, ISOLEUCINE, THREONINE,
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copyright. It is produced tute of Bioinformatics and
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Sciurognathi; Muridae;
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Best Local
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                                                                                                                                             MEDLINE-89296507; PubMed-274U23;
Lamhonwah A.-M., Mahuran D.J., Gravel R.A.;
Lamhonwah A.-M., Mahuran D.J., Gravel R.A.;
"Human mitochondrial propionyl-CoA carboxylase:
N-terminus of the pro- and mature alpha chains i
primary sequence of a full-length cDNA.";
primary sequence of a full-length cDNA.";
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BINDING
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                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Last sequence upon 16-OCT-2001 (Rel. 40, Last annotation prophonyl-CoA carboxylase alpha chain, (EC 6.4.1.3) (PCCase alpha subunit) (P)
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                                                       SEQUENCE FROM N.A.
                                                                                                                                     REVISIONS.
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A34337; A34337.
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26; Conservative
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PS00866; CPSASE_1; 1.
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 (NOV-2000)
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biotin_lipoyl; 1.
Biotin_carb_C; 1.
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in, mitochondrial precursor
(Propanoyl-CoA:carbon dioxide
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EMBL;
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the Euro
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MOI. Genet. Metab. 67:11-22(1999).

-i- CATALYTIC ACTIVITY: ATP + propanoy1-CoA + HCO(3)(-) = phosphate + (S)-methylmalony1-CoA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lamhonwah A.-M., Quan F., Gravel R.A.; "Sequence homology around the biotin-binding site of human propionyl-CoA carboxylase and pyruvate carboxylase."; Arch. Biochem. Biophys. 254:631-636(1987).
                                                                                                         modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99433966; PubMed-10502773;
Ugarte M., Perez-Cerda C., Rodriguez-Pombo
Richard E., Muro S., Campeau E., Ohura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [4]
SEQUENCE OF 344-5:
MEDLINE=86259695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99263311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS PA-1 P-50; K-204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99203168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS PA-1 W-52; T-113; T-139;
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of enzyme de
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lamhonwah A.-M., Bara
Quan F., Gravel R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 loning of functional alpha propionyl CoA carboxylase enzyme deficiency in pccA fibroblasts."; J. Hum. Genet. 52:144-151(1993).
                                                                                                                                                                                            ALPHA SUBUNITS AND SIX BETA SUBUNITS:
SUBCELLULAR LOCATION: MICOCHONDIAI matrix.
DISEASE: DEFECTS IN PCCA ARE THE CAUSE OF PROPIONIC ACIDEMIA, [1]
[PA-1], A LIFE-THREATENING DISEASE CHARACTERIZED BY EPISODIC VOMITING, LETHARGY AND KETOSIS, NEUTROPENIA, PERIODIC THROMBOCYTOPENIA, HYPOGAMMAGLOBULINEMIA, DEVELOPMENTAL RETARDATION, AND INTOLERANCE TO PROTEIN.
                                                                                                                                                                                                                                                                                                   PATHWAY: KEY ENZYME IN THE CATABOLIC PATHWAY OF FATTY ACIDS, ISOLEUCINE, THREONINE, METHIONINE, SUBUNIT: PROBABLY A DODECAMER COMPOSED OF SIX B
                                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                 SWISS-PROT entry is copyright.
   X14608; CAA32763.1; -. BC000140; AAH00140.1; M13572; AAA60035.1; -. S55656; AAB25345.1; -.
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                                                                        s requires a license agreement (See http://www.isb-sib.
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 instability of the protein.";
. Biophys. Acta 1453:351-358(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  defects:
                                                                                                  SS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the Expean Bioinformatics Institute. There are no restranon-profit institutions as long as its content and this statement is not removed. Usage by and
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defects: identification of five novel
lnstability of the protein.":
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PubMed=3555348;
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Pfam; PF00785; Blotin_carb_C; 1.
Pfam; PF02785; CPSase_L_D2; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00866; CPSASE_1; 1.
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Q974#8 sulfolobus
Q974#8 sulfolobus
Q92cwl listeria mo
Q98986 bacillus ha
Q99216 streptococc
Q8r912 corynebacte
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Q99218 sapergillus
Q97264 streptomyce
Q92207 racidaminoco
Q90267 lactococcus
Q9129 pseudomonas
P94468 bacillus st
Q9664 streptomyce
Q92207 racidaminoco
Q90chq7 lactococcus
Q9129 pseudomonas
P95127 mycobacteri
Q9213 rhizobium l
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Q9310 caulobacteri
Q9113 rhizobium e
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Methylmalonyl-CoA decarboxylase gamma chain.
     SEQUENCE FROM N.A
                                                                                 Pyrococcus.
                                                                                                          Pyrococcus horikoshii.
Archaea; Euryarchaeota;
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InterPro; IPR00088; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl; 1.
PROSITE; PS00188; BIOTIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJZ48285; CAB49799.1; -.
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Archaea; Euryarchaeota;
                                                           NCBI_TaxID=53953;
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5 Q19842
16 Q99TW6
2 Q54761
1 Q9HH18
2 Q9XCV7
2 Q54119
2 Q54119
2 Q54119
16 Q8YJ20
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Q9A797
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Pred. No. 1.6e
10; Mismatches
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O9ry33 deinococcus
O18842 caenorhabdi
O99tw6 staphylococ
O54761 synechococc
O9h118 methanosarc
O9xcv7 streptomyce
O54105 saccharopol
O54105 saccharopol
O89j20 brucella me
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Q9a797 caulobacte
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  058564
058564;
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InterPro; IPR001089; Biotin_lipyl.
Pfam; PF00364; biotin_lipoyl; 1.
PROSITE; PS00188; BIOTIN; UNKNOWN 1
COMPLETE PROCESSES.
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Takamiya M., Ohfuku Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5.55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome. SEQUENCE 144 AA;
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01-JUN-2002 (TrEMBLrel. 21, Last ann
Methylmalonyl-CoAdecarboxylase gamma
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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HSSP; P10802; 11
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                                                                                                                                                                                                                                                                        VTAPMPGKILKILVSEGQRVTIGQGLLILEAMKMENEIPSPKDGVVKKIYVKEGDTVDTG 137
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                                                                                                                                                                                                                                                                                                                                                                                Similarity 55.;
37; Conservative
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                            PRELIMINARY;
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Pred. No. 4.2e-11;
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                            PRT;
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01-JAN-1998
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PROSITE; I
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01-JAN-1998 (TrEMBLrel. 05, Last
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Methylmalonyl-CoA decarboxylase,
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Pfam;
          STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE-98049343; PubMed-9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.
                                                                                    SEQUENCE FROM N.A.
STRAIN-VC-16 / DSN
                                                                                                                       Archaeoglobus fulgidus.
Archaea; Euryarchaeota;
Archaeoglobaceae; Archae
NCBI_TaxID-2234;
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InterPro; IPR003379; PYC_OADA.
Pfam; PF00334; biotin_lipoyl; 1.
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HSSP; P02905; 18D0
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Archaea; Euryarchaeota;
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PF02436; PYC_OADA; 1.
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tate decarboxylase
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i J., Kushida N.,
b F.T., Horikoshi
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Glodek A., Zhou
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01-AUG-1998
01-MAR-2002
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067484;
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Nature 390:364-370(1997).
EMBL; AE000952; AAB89036.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aquifex aeolicus.
Bacteria; Aquificae;
NCBI_TaxID=63363;
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InterPro; IPR000089; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl; 1.
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Cotton M.D., Spriggs T., Al
Sadow P.W., D'Andrea K.P.,
Mason T.M., Olsen G.J., Fra
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PF02436;
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PS00188; BIOTIN; UNKNOWN_1.
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IPR000089; Biotin_lipoyl.
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13; Mismatches
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                                                                                                                                        2839436F6BFE05D6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aquificaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keller M., Auj
                                                        DB 16;
.2e-09;
les 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McDonald L., Utterback
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                          Indels
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                                                                                                 655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.L.,
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GDVTPPMPGKVVKILVKEGEPVQQGQTVATVEAMKMENEVHAPIDGIVKKIFAKPGDQVN

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                                                                                                                                                                                                                                                                                  Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR000089; Biotin_lipoyl.
Interpro; IPR000991; CPSase.
Interpro; IPR000891; HMGL-like.
Interpro; IPR000891; HMGL-like.
Interpro; IPR000891; HMGL-like; 1.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF02786; Biotin_lipoyl; 1.
Pfam; PF02786; CPSase_L_D2; 1.
Pfam; PF02786; CPSase_L_D2; 1.
Pfam; PF02436; PMGL-like; 1.
Pfam; PF02436; PMGL-like; 1.
                                                      subunit
SSO2464.
                      Sulfolobus.
                              Sulfolobus solfataricus
Archaea; Crenarchaeota;
                                                               Biotin carboxyl carrier subunit (EC 6.4.1.3).
                                                                                  01-OCT-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                            Ligase.
          NCBI_TaxID=2287;
                                                                                                                     Q97VY7;
                                                                                                                               Q97VY7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99231848; PubMed-10217496; Okstad O.A., Hegna I., Lindbaeck T
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                TIGRFAMs; TIGR01235; pyruv_carbox; proSITE; PS00867; CPSASE_2; UNKNOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ010111; CAB40604.1;
HSSP; P24182; 1DV2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microbiology 145:621-631(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillaceae; Bac
NCBI_TaxID=1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus cereus.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9XBJ1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome organisation is not conserved
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                                                                                                                                                                                                                                                IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG
                                                                                                                                                                                                                         PDQAIMRI
                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                            TIGR01235;
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                                                                                                                                                                                                                                                                                                                 984 AA;
                                                                                                                                                                                                                                                                       Conservative
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(TTEMBLrel. 12, Last sequence update)
(TTEMBLEL. 21, Last annotation update)
rboxylase (EC 6.4.1.1) (Fragment).
                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                     CPSASE.
                                                                                                                                                                                                                                                                                  50.9%;
                                                                                                                                                                                                                                                                                                                110135 MW; 7AB52F8D453A147D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus/Clostridium group; Bacillales;
                                                        18, Created)
18, Last sequence update)
21, Last annotation update)
21 protein of propionyl-CoA carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lindbaeck T.,
                               Thermoprotei;
                                                                                                                                                                                                                                                                                                                                                Carbox; 1.
UNKNOWN_1
                                                                                                                                                                                                                                                                                           Score 174;
                                                                                                                                                                                                                                                                                  Pred.
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                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                               174; DB 2;
No. 1.9e-09;
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d between Bacillus cereus and
                                                                                                                              186
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                               Sulfolobales;
                                                                                                                              A
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                             Sulfolobaceae;
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Best Local S
Matches 34
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Best Local (
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01-NOV-1999 (
01-MAR-2002 (
                                                                                                                                                                                                                                         STRAIN-MSB8 / DSM 3109;

MEDLINB-99287316; PubMed-10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.S.

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White (
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.)

"Evidence for lateral gene transfer between Archaea and Bacteria
                                                                                                                                                                                                  genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
EMBL; AE001743; AAD35799.1; -.
                                                                                                               Complete proteome. SEQUENCE 134 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionyl-CoA
TM0717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A., De Moors A., Erauso G., Fletcher C., Gordon P.M.K., Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X. Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N., Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
                                                                                                                                          InterPro; IPROC
Pfam; PF00364;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Thermotoga maritima.
Bacteria; Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9WZH6
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                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001882; Biotin_attach.
InterPro; IPR000089; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl. 1.
PROSITE; PS00188; BIOTIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome of the crenarchaeon Proc. Natl. Acad. Sci. U.S.A. 98:7835-784 EMBL; AE006845; AAK42603.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-21332296; PubMed-11427726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
STRAIN-ATCC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177
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   83
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                4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG
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VKAPMAGIVLKVLVKEGQKVNVGDKLLVFEAMKMENELQSEFSGTVKEILVKEGDNIETG
                                                                                                                                                                        P02905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKGDILIVI 185
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                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. E 186 AA; 21166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                         IPR000089; Biotin_lipoyl
0364; biotin_lipoyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Thermotogae;
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                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carboxylase,
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                                                                                                                  Ā
                                                                                                                15131 MW;
                                                                      48.8%;
51.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12,
12,
20,
                                                       12;
                                                      Score 167; DB Pred. No. 1.1e
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                A3BFBAACE8574EC1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                annotation subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134
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7.6e-10;
hes 22;
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                                                                                  16;
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, Garrett M.M.,
, Richardson D.,
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                                                      Gaps
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RESULT Q97ER7 ID Q97ER7 Q97ER7 Q97ER7 Q97ER7 Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97ER Q97
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Best Local S
Matches 35
                                                                                                                   O97FR7 PRELIMINARY;
O97FR7;
O1-OCT-2001 (TremBLrel. 18, C
01-OCT-2001 (TremBLrel. 21, I
01-JUN-2002 (TremBLrel. 21, I
Pyruvate carboxylase, PYKA.
CAC2660.
                                                        Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium
Clostridiales; Clostridiaceae; Clostridium.
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Bacteria; Proteobacteria;
Legionellaceae; Legionell;
NCBI_TaxID=446;
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q48826;
    SEQUENCE
                                      NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biotin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hacker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 QILMKI 133
                                                                                                                                                                                                                                                                                                                                       586
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                                                                                                                                                                                                                                                                                                                                                                                                              PGQVLIRV
                                                                                                                                                                                                                                                                                                                                                                       GGQGLIKI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF02436; PYC_OADA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00364; biotin_lipoyl; PF00682; HMGL-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00165; DEHYDRATASE_SER_THR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR01108; oadA; PS00188; BIOTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brand
    FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000634; S/T_dehydrtse
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IPR000891;
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                                                                                                                                                                                                                                                                                                                                     593
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C., Lueck P.C., Di Bevardino
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HMGL-like.
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, Last annotation update)
alpha-chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 167; DB Pred. No. 5.8e 12; Mismatches
                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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5.8e-09;
21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           influences
.";
                                                                               Clostridia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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InterPro; IPR00379; PYC_OADA.
Pfam; PF02785; Biotin_Carb_C; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00289; CPSase_L_Chain; 1.
Pfam; PF002786; CPSase_L_D2; 1.
Pfam; PF00682; HMGL-llke; 1.
Pfam; PF00682; PYC_OADA; 1.
                                                                                                                                                                                                                                                            01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC 824 /
MEDLINE-21359325;
Noelling J., Breto
Gibson R., Lee H.M
cholerae.";
Nature 406:477-483(2000).
Nature 406:477-483(2000).
-i-COFACTOR: BIOTIN (BY SI)
EMBL; AE004141; AAF93718.1;
HSSP; P02905; 1BDO.
                                                                  SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwi
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                        1137
                                                                                                                                                                                                                                                                                                                                                                                                                       1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00481; POLITIAC; 1.
TIGRFAMS; TIGR01235; pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN; UNKNOWN_1.
                                                                                                                                                                                                   Bacteria; Proteobacteria;
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                Q9KUH1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tatusov R.L., Sabathe F., Doucette-Stamm L.,
Bennett G.N., Koonin E.V., Smith D.R.;
                                                  "DNA sequence
                                                                                                                                                                                                                            Vibrio cholerae
                                                                                                                                                                                                                                                    Oxaloacetate
                                                                                                                                                                                                                                                                                                              Q9KUH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence and comparative analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                   EIGASIPGNVVKVFVKPGDKVKKGDSLAVIEANKMETNVSVSEDGTVGGIFVKEGDQVQS 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Similarity
34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteome
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IPR000891; HMGL-like.
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                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9325; PubMed=11466286;
Breton G., Omelchenko
                                                                                                                                                                                                                                                                                                                                                                                              69
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                                                           of both
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                                                           chromosomes
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                        SIMILARITY).
                                                                                                                                                                                                                gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNKNOWN_1.
                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 167; DB 16;
Pred. No. 1.2e-08;
1; Mismatches 22;
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                                                           of the
                                                                                                                                                                                                                                                                                                              597
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                                                           cholera
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                                                          pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1144;
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                                                                                yam L.A.,
son D.,
son Sellers !
, white O.,
'enter
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                                                                                                      P.,
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RESULT OPPOUT OF PRODUCT OPPOUT 
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Best Loc
Matches
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InterPro: IPR003379; PYC_oADA.
InterPro: IPR003379; PYC_oADA; 1.
Pfam: PF000882; HugL-like; 1.
Pfam: PF00682; HugL-like; 1.
Pfam: PF02436; PYC_oADA; 1.
ITGRRAMs; TIGR01108; OadA; 1.
PROSITE; PS00188; BIOTIN; 1.
Biotin; Complete proteome.
                                             529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN-NCTC 11168;

MEDLINE-20150912; PubMed-10688204;

Parkhill J., Wren B.W., Mungall K., Ketley J.M., Church,

Basham D., Chillingworth T., Davies R.M., Feltwell T.,

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn on the sequence of the food-borne pathogen Campylo

"The genome sequence of the food borne pathogen Campylo"
                                                                                                                                                                                                                      rram; PP00682; HMGL-līke; 1.
PROSITE; PS00188; BIOTIN; 1.
Biotin; Complete proteome.
SEQUENCE 599 AA; 65833 MW
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                reveals hypervariable sequences.";
Nature 403:665-668(2000).
-!- COFACTOR: BIOTIN (BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyca or CJ0933C.
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL139076; CAB73190.1;
HSSP; P20708; 1GHJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campylobacter jejuni.
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                                                                                                                                                               Local
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QGGQGL 66
                                                                             EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
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                                             ENEVLAGISGNVFKIYVNEGEEVKSGQAIMVLEAMKMEIEVNAPKDGIILELCIKIGDTV
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                                                                                                                                                                                                                                                                                                   PF00364; biotin_
PF00682; HMGL-li
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E 597 AA; 64795 MW;
                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                               IPR001882; Biotin_attach.
IPR000089; Biotin_lipoyl.
IPR000891; HMGL-like.
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                          47.7%;
                                                                                                                                                                                                                                  65833 MW;
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HMGL-like.
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Pred. No. 1.5e
13; Mismatches
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4; Mismatches
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1,2e-08;
ches 19;
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les 20;
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C.W.,
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Best Local
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01-JAN-1998
01-MAR-2002
                                                                                                                                                   Q8U917;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Richardson D.L., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Springer J.D., Weidman J.F., McDonald L., Utterback T.,
 SEQUENCE FROM N.A.
MEDLINE=21608550; PubMed=11743193;
Wood D.W., Setubal J.C., Kaul R., Okura V.K., Zhou Y., Chen L., Wood
                                                                                     Agrobacterium tumefaciens
Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
                                                                                                                           Biotin carboxylase.
ATU3913 OR AGR_L_1864.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00364; biotin_lipoyl; 1
Hypothetical protein; Complete
SEQUENCE 142 AA; 15573 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL; AE000960; AAB89171.1; -.
HSSP; P10802; IIYU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                              Q8U917
                                                                       NCBI_TaxID=176299;
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MEDLINE=98049343; PubMed=9389475;
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(TrEMBLrel. 05,
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e decarboxylase,
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  Kaul R., Mun L., Wood (
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                                                                                                (strain C58 / ATCC alpha subdivision;
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Last sequence up
Last annotation
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biotin carboxyl carrier subunit, putative.
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3; Mismatches
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73439FBD49E469A1 CRC64;
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  Monks D.
od G.E., A
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    Almeida N.F.
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Rhizobiaceae
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Best Local 9
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EMBL; RE008669; AALO3497.1; ...
InterPro; IPR001882; Biotin_attach.
InterPro; IPR001882; Biotin_lipoyl.
InterPro; IPR001089; Biotin_lipoyl.
InterPro; IPR0010901; CPSase.
Pfam; PF02785; Biotin_lipoyl; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00289; CPSase_L_Chain; 1.
Pfam; PF02786; CPSase_L_D2; 1.
PROSITE; PS00188; BIOTIN; UNKNOWN_1.
PROSITE; PS001866; CPSASE_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the plant payrobacterium tumefaciens C58. Science 294:3233-3238 (2001).
EMBL; AE009322; AAL44721.1; -. EMBL; AE008292; AAK89506.1; -.
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Qurollo B.,
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Raoult D.;
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PCCa OR RC0959
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                                                                                                                                                                                                                                  Science
                                                                                                                                                                                                                                                                                                                          MEDLINE-21442074; PubMed-11557893; Ogata H., Audic S., Renesto-Audiff
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Roux V.,
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eae; Rickettsia.
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Pred. No. 3.3e
13; Mismatches
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Matches 34
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Best Local :
                          09HTD1;
01-MAR-2001
01-MAR-2001
01-JUN-2002
Probable trai
                                                                                                                                                                                                                                                                                                     Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takaniya Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagish Oshima T., Kikuchi H.;
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01-DEC-2001
01-JUN-2002
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                                                                                                                                                                                                                                                                                "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA RES. 8:123-140(2001).
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                                                                           Q9HTD1
                                                                                                                                                                                                                                             InterPro; IPR000089; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl; 1.
Hypothetical protein; Complete prot
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Pseudomonas
Bacteria; P
                   PA5435.
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Proteobacteria;
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         aeruginosa
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Pred. No. 4.3e-08;
2; Mismatches 21;
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Pred. No. 1.2e-08;
2; Mismatches 23;
                                                                          PRT;
                                                                                                                                                                                                                                    proteome.
4F1D96761F5BE3DD CRC64;
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subdivision;
                                    annotation
                                              sequence
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                                    update)
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Pseudomonadaceae;
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RESULT 19
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ID Q92CW
AC Q92CW
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RA Barguero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Demann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Ra Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Ra Comparative genomics of Listeria species.";
Science 294.849-852(2001).
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CSTRAIN-ATCC 15692 / PAO1;

XX MEDLINE-20437337; PubMed-10984043;

XX MEDLINE-20437337; PubMed-10984043;

XX Hickey M.J., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

XX Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

XX Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

XX Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

XX Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

XX Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

**Complete genome sequence of Pseudomonas aeruginosa PAO1, an

**Opportunistic pathogen.**;

VY Opportunistic pathogen.**;

VY Nature 406:959-964(2000).

XX EMBL, AEO04955, AAROB820.1;

XX PASSP: P02905; 3BDO.
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Best Loc
Matches
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InterPro; IPR000891; HMGL-like.
InterPro; IPR003379; PYC_OADA.
InterPro; IPR000631; S/T_dehydrtse.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00682; HMGL-like; 1.
Pfam; PF00436; PYC_OADA; 1.
TIGRFAMS; TIGR01108; oadA; 1.
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Bacteria; Firmicutes;
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PYCA OR LIN1060
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01-JUN-2002
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01-DEC-2001
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NCBI_TaxID=1642;
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NCBI_TaxID=287;
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Pred. No. 4.9e
12; Mismatches
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Last annotation update)
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1.9e-08;
1es 23;
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RA Glaser P., Frangeul L., Buchrisser C., Rusniok C., Amend A.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Maddeno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Maddeno E., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Nacquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RT "Comparative genomics of Listeria species.";
RI Science 294:849-852(2001).
DR EMBL; AL59197; CAC99150.1; -.
DR Listilist; LM001072; -.
DR Listilist; LM001072; -.
DR Listerio IPR000901; CPSase.
DR InterPro; IPR000901; CPSase.
DR InterPro; IPR000901; CPSase.
DR InterPro; IPR003379; PYC_OADA.
DR Pfam; PP02785; Biotin_carb_C; 1.
DR Pfam; PP02786; CPSase_L_Chain; 1.
DR Pfam; PF02786; CPSase_L_Chain; 1.
DR Pfam; PF02786; CPSase_L_Chain; 1.
DR Pfam; PF02786; TGR01235; pyruv_carbox; 1.
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Best Local S
Matches 29
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01-MAR-2002
01-MAR-2002
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Pfam;
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NCBI_TaxID=1639;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
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PROSITE; PS00866; CPSASE_1; UNKNOWN_1
PROSITE; PS00867; CPSASE_2; UNKNOWN_1
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Pfam;
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InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000901; CPSase.
InterPro; IPR000891; HMGL-like.
InterPro; IPR00379; PYC_OADA.
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PF00264; biotin_lipoyl; 1.
PF00289; CPSase_L_chain; 1.
PF002786; CPSase_L_D2; 1.
PF00682; HMGL-like; 1.
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Pred. No. 1
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InterPro; IPR000901; CPSase.
InterPro; IPR000891; HMGL-like.
InterPro; IPR003379; PYC_OADA.
Pfam; PF002785; Biotin_carb_C; 1.
Pfam; PF00284; biotin_lipoyl; 1.
Pfam; PF00289; CPSase_L_chain; 1.
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PROSITE;
Complete
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Bacteria; Firmicutes;
Bacillaceae; Bacillus.
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MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R.
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9К9М0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9K9M0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1138 DLLIEV 1143
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                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P24182; 1BNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of the alkaliphilic bacterium Bacillus nalodurans and genomic sequence comparison with Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                     22
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                                                                                                                                   64 QGLIKI 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63 : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGATMTGSVIQVVVKKGDSVKKGDPLLITEAMKMETTIQAPFDGEVSSIYVSDGDTIESG 1137
                                                                                                                                                                              IGASMPGTVVKALVEKGDKVKQGDHLMITEAMKMETTVQAPFDGEVVALHVKDGDAIQTG 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF02436;
                                                                                                                                                                                                                                                                           33; Conserv
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1146 AA;
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1150 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                           PS00867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000089; Biotin_lipoyl.
                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAB06344.1;
                                                                                                                                                                                                                                                                                                                                                                                                       CPSASE_2; UNKNOWN_1
                                                                                                                                                                                                                                                                                         45.9%;
50.0%;
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UNKNOWN_1.
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                                                                                                                                                                                                                                                                      Score 157; DB 16;
Pred. No. 1.3e-07;
3; Mismatches 20
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Pred. No. 1.3e-07;
7; Mismatches 20
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                                                                                                                                                                                                                                                                                                                                                                ED6788BE8A9F3BD4 CRC64;
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                                                                                                                                                                                                                                                                                                                   DB 16;
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RESULT 23
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                                                                                                                                                                      PYC.
Corynebacterium efficiens.
Corynebacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q99ZL6 PRELIMINARY;
Q99ZL6;
Q1-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                  Q8RQL2;
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Biotin; Lyase; Complete proteome
SEQUENCE 116 AA; 12288 MW; A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: BIOTIN (BY SIMILARITY).
EMBL; AE006558; AAK34043.1; -.
HSSP; P02905; 1BDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SF370 / ATCC 700294 / SEROTYPE MEDLINE-21192684; PubMed-11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium
Streptococcaceae; Streptococcus.
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InterPro; IPR00089; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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01-MAR-2002
                                                   SEQUENCE
                                                                           Submitted (APR-2002)
                                                                                                               SEQUENCE FROM N.A.
Akiyoshi N., Nonaka G.,
                                                                                                                                                     NCBI_TaxID=152794;
                                                                                                                                                                  Corynebacterium.
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                                                                                               Corynebacterium efficiens pyruvate
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                                                                                                                                                                                                                                                                                                                                                                                     63 GQGLI 67
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                                                                                                                                                                                                                                                                                                                                                            EQVLI 114
                                                  AB083299; BAB88903.1; -.
NCE 1139 AA; 123068 MW;
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              Similarity
                                                                                                                                                                                                                                carboxylase.
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  Conservative
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                                                                                                                                                                                                                                                                                               PRELIMINARY;
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             45.58;
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                                                                                                               Kimura E.,
  15;
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Last annotation update
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Pred.
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Pred. No. 1
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Mismatches
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                                                   BA7023134519FAAA CRC64;
                                                                                                               Kawahara Y.,
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                         155.5;
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                                                                                                   carboxylase
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                         DB 2;
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                                                                                                               Sugimoto S.;
                                                                                                  (pyc) gene,
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                       Length 1139;
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Q8RAJ2 PRELIMINARY
Q8BAJ2;
01-JUN-2002 (TrEMBLiel.
                                                                                                                                                                                              Pfam;
Pfam;
                                                       1131
                                                                                   1072
                                                                                                                                                  TIGRFAMS; TIGR01235; pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
Biotin; Ligase; Pyruvate;
                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                              EMBL; AF038548; AAB92588.
EMBL; Y09548; CAA70739.1;
HSSP; P24182; 1BNC.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ATCC 13032;
Peters-Wendisch P.G.,
                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1130
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                                                                                                                                                                                                                                                                                           Submitted (FEB-1998)
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                                                                                                                                                                                                                                                                                                                                             Stephanopoulos
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Corynebacterium.
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01-JUN-1998
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                                                                                                                                                                                                                                  interPro;
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                                                                                                                      Local
                                                                                                                              Match
                                                                                                                                                                              erPro; IPR000891; HMG1-like.
erPro; IPR003879; PYC_OADA.
m; PF02785; Blotin_carb_C; 1.
m; PF00304; blotin_lipoyl; 1.
m; PF000389; CPSase_L_chain; 1.
m; PF00089; CPSase_L_D2; 1.
m; PF00089; CPSase_LLD2; 1.
m; PF00089; HMG1-like; 1.
m; PF00089; PYC_OADA; 1.
                                                                                                                                                                                                                                                                                    COFACTOR: BIOTIN
                                                                     QGGQGLIKI
                                                                                               EGETPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV
                                                      EGGDLIVVV 1139
                                                                                   KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVPAATKV
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                                                                                                                                             1140
                                                                                                               Conservative
                   PRELIMINARY;
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                                                                                                                                            123102 MW;
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                 PRT;
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smatches 23;
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01-UN-2002 (TIEMBLEEL. 21, Las. ...
Biotin carboxyl carrier protein.
ACCD OR TIE122.
Thermoanaerobacter tengcongensis.
Thermoanaerobacter tengcongensis.
Thermoanaerobacter tengcongensis.
Thermoanaerobacter tengcongensis.
Thermoanaerobacter flostridia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998
01-AUG-1998
01-JUN-2002
              Pfam;
Pfam;
                                               InterPro: IPR002453; Beta_tubulin. InterPro: IPR001882; Biotin_attach. InterPro: IPR0010889; Biotin_lipoyl. InterPro: IPR000891; HMGL-like. InterPro: IPR003379; PYC_OADA. Pfam; PF00364; biotin_lipoyl; 1.
                                                                                                                                                        -:- COFACTOR: BIOTIN (BY SIMILARITY)
-:- SIMILARITY: BELONGS TO THE TUBUL
EMBL, AE000747; AEC07497.1; -.
HSSP; P02905; 1BDO.
                                                                                                                                                                                                                                         Nature 392:353-358(1998).
-!- FUNCTION: TUBULIN IS
BINDS TWO MOLES OF GT
CHAIN AND ONE AT A NO
                                                                                                                                                                                                                                                                                                                           Deckert G., Warren P.V., Gaasterland T., Young W.G., Ler Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay N. Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., D
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X
Tan H., Chen R., Way Y., Lu Y., Yang H.;
"A complete sequence of T. tengcongensis genome.
Genome Res. 12:689-700(2002).
EMBL, AE013084; AAM24452.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aquifex aeolicus.
Bacteria; Aquificae;
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                                                                                                                                                                                                                                                                                                                  aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98196666; PubMed=9537320;
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                PF00682;
PF02436;
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            ; biotin_lipoyl;
; HMGL-like; 1.
; PYC_OADA; 1.
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oadA;
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GTP, ONE AT AN EXCHANGEABLE SITE ON THE I
NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN
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es 23;
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Huber
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RESULT
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Q40121;
Q40121;
Q1-NOV-1996 (TrembLrel. 01, Created)
Q1-NOV-1996 (TrembLrel. 01, Last sequence update)
Q1-UN-2002 (TrembLrel. 21, Last annotation update)
Q1-UN-2002 (TrembLrel. 21, Last annotation update)
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PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.
Biotin; GTP-binding; Microtubules; Comp
                                       Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptoph;
Spermatophyta; Magnoliophyta; eudico
Asteridae; euasterids I; Solanales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burton N.P., Williams T.D., Norris P.R., "Carboxylase genes of Sulfolobus metalli Arch. Microbiol. 172:349-353(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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  SEQUENCE FROM N.A.
                          NCBI_TaxID=4081;
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                                                                                                                                                                                                                                                                                     EGEVLSPLOGRVVAIRVKEGDAVTKGQPLLSVEAMKSETIISAPIAGVIEKIAVKPGQGV 157
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NCE 167 AA; 18580 MW;
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50.78;
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                                     Streptophyta; Embryophyta; Tracheo yta; eudicotyledons; core eudicots; Solanales; Solanaceae; Solanum.
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Pred. No. 1.6e-07;
4; Mismatches 23
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4F306D48794AE859 CRC64;
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                                                                                                                                                                                                                                                              TIGREAMS;
PROSITE; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SF370 / ATCC 700294 / SEROTYPE M1;
MEDLINE-21192604; Pubmed-11296296;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
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-I- COFACTOR: BIOTIN (BY SIMILARITY).
EMBL; U07745; AAA19157.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang X:, Wurtele E.S., Keller G., McK "Molecular cloning of cDNAs and genes COA carboxylase of tomato.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an Ml strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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                                                                                                                                                                                                                                                                                                                                              Pfam; PF00364; biotin_lipoyl; PRINTS; PR01071; ACOABIOTINCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE006603; AAK34491.1; -.
HSSP; P02905; 1BDO.
InterPro; IPR001249; AcCoA_biotinCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-SF370 / ATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcaceae;
NCBI_TaxID=1314;
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InterPro; IPR000089; Biotin_lipoyl.
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SEQUENCE FROM N.A.

SEQUENCE-125 / JCM 9153;

KE STRAIN-C-125 / JCM 9153;

MEDLINE-20512582; PubMed-11058132;

MEDLINE-20512582; PubMed-11058132;

WA Fuji F., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,

Na Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,

Horikoshi K.;

"Complete genome sequence of the alkaliphilic bacterium Bacillus and denomic sequence comparison with Bacillus subtilis.";

Na Complete genome sequence comparison with Bacillus subtilis.";

Nucleic Acids Res. 28:4317-4331(2000).

EMBL; APO01511; BAB04852.1; -

NR HSSP; P10802; 1IYU,

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HSSP; P10802; 1IYU,

MEDLINE-2051258

SEQUENCE 70 AA; 7563 MW; 6A6AC14B14B5F7AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 43.9
Best Local Similarity 46.3
Matches 31; Conservative
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O9KDS8;

01-OCT-2000 (TrEMBLrel. 15, Created)

01-OCT-2000 (TrEMBLrel. 15, Last sequ

01-MAR-2002 (TrEMBLrel. 20, Last anno

Hypothetical protein BH1133.
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NCBI_TaxID=86665;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
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149 LVSNEDVIEFGQGLVRI 165
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 150; DB 16; Length 70; Pred. No. 2.8e-08; 5; Mismatches 21; Indels
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